

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 05:35:40 ; Search time 8243 Seconds

(without alignments)
17617.736 Million cell updates/sec

Title: US-09-676-436-3

Perfect score: 1 ctaagaactctccgatga.....ggttaatttagaagaagtc 4990

Sequence: IDENTITY NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 993650

Minimum DB seq length: 8

Maximum DB seq length: 100

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 1000 summaries

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Database :
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2: gb_ba:*
3: gb_hlg:*
4: gb_in:*
5: gb_om:*
6: gb_ov:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_yi:*
15: em_da:*
16: em_hum:*
17: em_in:*
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40: em_mu:*
41: em_mu:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	29.6	0.6	87	3	DDIDDKD	M59747 D. discoiden
2	26	0.5	100	6	AR007403	AR007403 Sequence
3	25.8	0.5	81	6	AX381834	AX381834 Sequence
4	25.4	0.5	96	5	AF025984	AF025984 Paratich
5	25.2	0.5	65	6	AX486379	AX486379 Sequence
6	25.2	0.5	70	1	AX033167	AX033167 Sequence
7	25.2	0.5	70	6	AX033159	AX033159 Sequence
8	25.2	0.5	99	6	165769	165769 Sequence 5
9	24.8	0.5	83	4	RABPFKM18	M14473 Rabbit musc
10	24.8	0.5	92	6	AX173377	AX173377 Sequence
11	24.6	0.5	71	6	AR140801	AR140801 Sequence
12	24.6	0.5	71	6	193480	193480 Sequence 78
13	24.6	0.5	71	6	193480	193480 Sequence 78
14	24.6	0.5	73	3	AR203036	AR203036 Sequence
15	24.4	0.5	98	6	AR203036	AR203036 Sequence
16	24.4	0.5	98	6	AR203036	AR203036 Sequence
17	24.4	0.5	100	3	DROTRANSIN	AR007408 Sequence
18	24.2	0.5	65	6	AX486337	AX486337 Sequence
19	24	0.5	51	10	U92177	U92173 Mus musculu
20	24	0.5	65	6	AX486371	AX486371 Sequence
21	24	0.5	65	6	AX207310	AX207310 Sequence
22	24	0.5	88	6	AB04840511	AB048411 Homo sapi
23	24	0.5	97	6	AR014621	AR014621 Sequence
24	24	0.5	97	6	BD010413	BD010413 Chimeric
25	24	0.5	97	6	126754	126754 Sequence 54
26	24	0.5	97	6	AF294358	AF294358 Bos tauru
27	23.8	0.5	82	4	AF294358	AF294358 Bos tauru
28	23.8	0.5	87	14	AF050514	M28495 Trypanosoma
29	23.8	0.5	90	3	TRBANTATC2	AX130784 Mus muscu
30	23.8	0.5	91	10	MM0130784	AX130784 Mus muscu
31	23.8	0.5	94	6	AX326634	AX326634 Sequence
32	23.8	0.5	94	6	AX326671	AX326671 Sequence
33	23.8	0.5	94	6	S52152519	S52191 CD11b-Leuko
34	23.8	0.5	94	6	AF025985	AF025985 Paratich
35	23.8	0.5	96	5	AF025985	AF025985 Paratich
36	23.6	0.5	87	6	AR062856	AJ305430 Homo sapi
37	23.6	0.5	88	11	HUM07770A	AR062856 Sequence
38	23.6	0.5	98	6	AX326603	L31186 Human STRs
39	23.6	0.5	99	6	AX059602	AX326603 Sequence
40	23.6	0.5	100	6	AP025983	AX059602 Sequence
41	23.4	0.5	79	10	AX486370	AF025983 Paratich
42	23.4	0.5	80	6	AX240922	A20465 oligonucleo
43	23.4	0.5	83	6	AX240922	M32437 Rat/polyoma
44	23.4	0.5	83	6	S72771	AF480570 Homo sapi
45	23.4	0.5	88	6	AX015186	AX240922 Sequence
46	23.4	0.5	99	11	HSPE99C03	AX015186 Sequence
47	23.2	0.5	65	6	AX483262	AX013823 H.sapiens
48	23.2	0.5	87	4	CHRMILLAS	AX483262 Sequence
49	23.2	0.5	97	4	OCU072578	M19461 Chicken c-m
50	23.2	0.5	100	5	AF174523	U72578 Oryctolagus
51	23.2	0.5	89	17	HSEXR35	AF174523 Bufo dana
52	23	0.5	91	6	AX391840	T10934 H.sapiens D
53	23	0.5	90	6	HSU032336	AX391840 Sequence
54	23	0.5	94	6	AR170294	U32336 Human pre-B
55	23	0.5	94	6	AX007122	AR170294 Sequence
56	23	0.5	94	6	AX020432	AX007122 Sequence
57	23	0.5	94	6	E51068	AX020432 Sequence
58	23	0.5	98	14	AF292795	E51068 Novel Esche
59	23	0.5	100	9	HS4387E	AF292795 HIV-1 cto
60	22.8	0.5	100	9	HS4387E	Z58534 H.sapiens C
61	22.8	0.5	55	9	HSADDS24	AF000104 Homo sapi
62	22.8	0.5	55	10	S69914	S69914 BCL-2-RNA P
63	22.8	0.5	65	6	AX484094	AX484094 Sequence
64	22.8	0.5	76	6	A20466	A20466 oligonucleo
65	22.8	0.5	76	6	AR007324	AR007324 Sequence

C 66	22.8	0.5	85	11	AL807913	AL807913 Arabidops	C 139	21.8	0.4	65	14	SVANKV3	K08095 simian vlrn
C 67	22.8	0.5	90	9	HSREPAL3	X06682 Human DNA 1	C 140	21.8	0.4	66	9	HUMTCGDE	M28799 Human T-cell
C 68	22.8	0.5	94	3	BVU52988	U52988 Bonellia v1	C 141	21.8	0.4	73	6	A19086	A19086 Nucleotide
C 69	22.8	0.5	94	6	AX088804	AX088804 Sequence	C 142	21.8	0.4	73	9	AF147985	AF147985 Homo sapi
C 70	22.8	0.5	95	6	EO3691	EO3691 DNA Sequence	C 143	21.8	0.4	74	6	A19085	A19085 Nucleotide
C 71	22.8	0.5	96	6	AR107453	AR107453 Sequence	C 144	21.8	0.4	77	5	AX381381	AX381381 Nucleotide
C 72	22.8	0.5	96	10	MUSIGHF	M17054 Mouse Ig-G2	C 145	21.8	0.4	79	5	AF517937	AF517937 Labo dus
C 73	22.8	0.5	100	11	HUMUT1990A	L30649 Human STS U	C 146	21.8	0.4	79	6	AF145885	AF145885 Sequence
C 74	22.6	0.5	51	6	AX161521	AX161521 Sequence	C 147	21.8	0.4	79	6	AX003015	AX003015 Sequence
C 75	22.6	0.5	51	6	AX161523	AX161523 Sequence	C 148	21.8	0.4	80	6	AX146300	AX146300 Sequence
C 76	22.6	0.5	51	6	AX199647	AX199647 Sequence	C 149	21.8	0.4	81	6	AR110371	AR110371 Sequence
C 77	22.6	0.5	64	6	AX381699	AX381699 Sequence	C 150	21.8	0.4	81	6	BD009391	BD009391 Chimeric
C 78	22.6	0.5	69	9	AF189373	AF189373 Homo sapi	C 151	21.8	0.4	83	6	A19093	A19093 Nucleotide
C 79	22.6	0.5	69	9	APU09225	U09225 Alouatta pa	C 152	21.8	0.4	83	6	A19095	A19095 Nucleotide
C 80	22.6	0.5	87	10	MUSIGHL	M17767 Mouse Ig no	C 153	21.8	0.4	83	6	AX146299	AX146299 Sequence
C 81	22.6	0.5	87	14	AF050512	AF050512 Human end	C 154	21.8	0.4	85	14	SVANKM1	K08019 simian vlrn
C 82	22.6	0.5	93	3	HUMUT1990A	D32037 Human mRNA	C 155	21.8	0.4	86	6	A19096	A19096 Nucleotide
C 83	22.6	0.5	100	6	AX379183	M16930 Rat nucleins	C 156	21.8	0.4	87	6	A19094	A19094 Nucleotide
C 84	22.6	0.5	64	9	HSAT27172	AX379183 Sequence	C 157	21.8	0.4	94	10	MMVIMV73	X89190 M.musculus
C 85	22.6	0.5	81	14	AF227769	AX277769 Sequence	C 158	21.8	0.4	95	6	A33974	A33974 Synthetic P
C 86	22.4	0.4	81	14	AF227769	AF227769 Hepatitis	C 159	21.8	0.4	95	6	A77225	A77225 Synthetic P
C 87	22.4	0.4	90	9	CORINORFB	M69102 Gorilla end	C 160	21.8	0.4	96	6	A33975	A33975 Synthetic P
C 88	22.4	0.4	90	9	CORINORFB	A45371 Sequence 41	C 161	21.8	0.4	98	6	AX039308	AX039308 Sequence
C 89	22.4	0.4	95	6	AR061176	AB044117 Homo sapi	C 162	21.8	0.4	98	6	AX039517	AX039517 Sequence
C 90	22.4	0.4	95	6	AR061176	AB044117 Homo sapi	C 163	21.8	0.4	99	6	AX341452	AX341452 Sequence
C 91	22.4	0.4	95	6	HSW62H13	X86912 H.sapiens s	C 164	21.8	0.4	100	6	AX023626	AX023626 Sequence
C 92	22.4	0.4	96	9	AR044618	BD010410 Chimeric	C 165	21.8	0.4	100	6	AX039309	AX039309 Sequence
C 93	22.4	0.4	97	6	BD010410	M83367 Human Plasm	C 166	21.8	0.4	100	6	AX039518	AX039518 Sequence
C 94	22.4	0.4	97	6	BD010410	AX162466 Sequence	C 167	21.6	0.4	30	6	E33550	E33550 Gene encodi
C 95	22.4	0.4	98	9	HUMPCB03	AX165549 Sequence	C 168	21.6	0.4	30	6	E34277	E34277 Environment
C 96	22.4	0.4	51	6	AX162466	AX165549 Sequence	C 169	21.6	0.4	30	6	E34333	E34333 Environment
C 97	22.2	0.4	51	6	AX165549	AX165549 Sequence	C 170	21.6	0.4	51	6	AX158309	AX158309 Sequence
C 98	22.2	0.4	51	6	AX165549	AX165549 Sequence	C 171	21.6	0.4	51	6	AX158310	AX158310 Sequence
C 99	22.2	0.4	65	6	AX485386	S81023 Ig heavy ch	C 172	21.6	0.4	51	6	AX199319	AX199319 Sequence
C 100	22.2	0.4	68	9	S81023	AR058866 Sequence	C 173	21.6	0.4	60	6	AX467093	AX467093 Sequence
C 101	22.2	0.4	71	6	AR058866	AR058866 Sequence	C 174	21.6	0.4	65	6	AX483973	AX483973 Sequence
C 102	22.2	0.4	71	6	AR063592	AR063592 Sequence	C 175	21.6	0.4	73	5	ICPARA3	ICPARA3 Sequence
C 103	22.2	0.4	71	6	AR063592	AR063592 Sequence	C 176	21.6	0.4	78	10	U96706	U96706 M.musculus
C 104	22.2	0.4	73	8	YSCGEC50X	AR140982 Sequence	C 177	21.6	0.4	80	12	SYNFCU3A	SYNFCU3A Sequence
C 105	22.2	0.4	76	6	AK080171	M87373 Yeast Eco R	C 178	21.6	0.4	83	6	AX098165	AX098165 Sequence
C 106	22.2	0.4	82	3	AF323690	AF323690 Acropora	C 179	21.6	0.4	85	10	RM05767	RM05767 Sequence
C 107	22.2	0.4	83	6	AX020990	AX020990 Sequence	C 180	21.6	0.4	85	10	RM05767	RM05767 Sequence
C 108	22.2	0.4	85	6	AR054868	AR054868 Sequence	C 181	21.6	0.4	87	6	AX340193	AX340193 Sequence
C 109	22.2	0.4	87	6	AR061133	AR061133 Sequence	C 182	21.6	0.4	88	9	AF279140	AF279140 Homo sapi
C 110	22.2	0.4	87	6	AR211441	AR211441 Sequence	C 183	21.6	0.4	90	8	AF479899	AF479899 Saccharom
C 111	22.2	0.4	90	9	S82667	S82667 Sequence 3	C 184	21.6	0.4	92	5	CHRCWBA3	CHRCWBA3 Sequence
C 112	22.2	0.4	90	9	S82667	S82667 Sequence 3	C 185	21.6	0.4	93	6	I74772	I74772 Chicken c-m
C 113	22.2	0.4	92	11	G37815	G37815 ACT1 Plasm	C 186	21.6	0.4	95	5	AF033547	AF033547 Luscinia
C 114	22.2	0.4	92	10	MMU03545	AX1403345 M.musculu	C 187	21.6	0.4	96	9	HSFHC09	HSFHC09 Sequence
C 115	22.2	0.4	94	6	AX134535	AX134535 Sequence	C 188	21.6	0.4	97	6	A77346	A77346 Human liver
C 116	22.2	0.4	94	6	AX326633	AX326633 Sequence	C 189	21.6	0.4	97	10	MSU05685	MSU05685 Sequence
C 117	22.2	0.4	94	6	AX326658	AX326658 Sequence	C 190	21.6	0.4	98	9	HSAPAE12	HSAPAE12 Arabidops
C 118	22.2	0.4	100	6	AX020439	AX020439 Sequence	C 191	21.6	0.4	100	9	MMU03452	MMU03452 M.musculu
C 119	22.2	0.4	40	9	AB076378	AB076378 Homo sapi	C 192	21.6	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 120	22.2	0.4	65	6	AX486026	AX486026 Sequence	C 193	21.6	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 121	22.2	0.4	65	6	AX486026	AX486026 Sequence	C 194	21.6	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 122	22.2	0.4	73	6	AX080404	AX080404 Sequence	C 195	21.6	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 123	22.2	0.4	78	10	MUSICAVB	M37592 Mouse T cel	C 196	21.6	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 124	22.2	0.4	81	6	A65654	A65654 Sequence 3	C 197	21.6	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 125	22.2	0.4	91	8	YSCATP041	J01518 Yeast (S.ce	C 198	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 126	22.2	0.4	92	6	AX388866	AX388866 Sequence	C 199	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 127	22.2	0.4	93	10	CRUGP102	M23800 Chinese ham	C 200	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 128	22.2	0.4	94	8	YSCGEC2X	M14022 T.Prncei (I	C 201	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 129	22.2	0.4	95	11	HSPEIAE07	AL009523 H.sapiens	C 202	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 130	22.2	0.4	96	10	MUSIGHCF	K02133 Mouse Ig ac	C 203	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 131	22.2	0.4	98	6	AX326604	AX326604 Sequence	C 204	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 132	22.2	0.4	98	11	HSPE75F09	AX326665 Sequence	C 205	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 133	22.2	0.4	100	9	HUMPTHEP1	AL0034309 H.sapiens	C 206	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 134	22.2	0.4	54	6	AR039666	D10291 Homo sapien	C 207	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 135	22.2	0.4	56	9	HUMNTCOP02	AR039666 Sequence	C 208	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 136	21.8	0.4	64	11	HUMUT646A	U84641 Human putat	C 209	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 137	21.8	0.4	64	11	HUMUT646A	L30064 Human STS U	C 210	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops
C 138	21.8	0.4	64	11	HUMUT646A	L30064 Human STS U	C 211	21.4	0.4	100	9	HSAPAE12	HSAPAE12 Arabidops

212	21.4	0.4	81	14	AF018313	AF018313 Hepatitis	285	21	0.4	50	3	GIANK33	LA9332 STS of NotI
213	21.4	0.4	84	6	A94799	A94799 Sequence 43	286	21	0.4	51	6	AX117257	AX117257 Sequence
214	21.4	0.4	84	6	A95594	A95594 Sequence 9	287	21	0.4	51	14	HIV1045085	HIV1045085
215	21.4	0.4	84	6	E03577	E03577 DNA sequence	288	21	0.4	55	6	A93058	A93058
216	21.4	0.4	89	8	AF001054	AF001054 GigaSpora	289	21	0.4	60	6	AR051992	AR051992
217	21.4	0.4	90	6	AR170725	AR170725 Sequence	290	21	0.4	60	6	AR060399	AR060399
218	21.4	0.4	90	6	AX114637	AX114637 Sequence	291	21	0.4	60	6	AR074851	AR074851
219	21.4	0.4	90	6	AX114763	AX114763 Sequence	292	21	0.4	60	6	AR078848	AR078848
220	21.4	0.4	90	6	AX118692	AX118692 Sequence	293	21	0.4	60	6	AR128957	AR128957
221	21.4	0.4	90	6	AX128109	AX128109 Sequence	294	21	0.4	60	6	E65257	E65257
222	21.4	0.4	90	6	E12579	E12579 Probe, 4/19	295	21	0.4	62	9	S52152831	S52152831
223	21.4	0.4	90	6	E12580	E12580 Probe, 4/19	296	21	0.4	65	6	AX484026	AX484026
224	21.4	0.4	90	6	E13639	E13639 Probe, 4/19	297	21	0.4	65	6	AX485310	AX485310
225	21.4	0.4	90	6	E17120	E17120 DNA probe.	298	21	0.4	65	6	AX485904	AX485904
226	21.4	0.4	90	8	AF317945	AF317945 Arabidops	299	21	0.4	65	6	AX486079	AX486079
227	21.4	0.4	92	5	AF420513	AF420513 Salmo sal	300	21	0.4	66	6	AX167457	AX167457
228	21.4	0.4	93	6	AR209741	AR209741 Sequence	301	21	0.4	72	9	AF043873	AF043873
229	21.4	0.4	95	10	HMCFTR12	HMCFTR12	302	21	0.4	73	6	AX233516	AX233516
230	21.4	0.4	95	10	MMU0403408	MMU0403408	303	21	0.4	74	6	AR011572	AR011572
231	21.4	0.4	97	6	A74708	A74708 Sequence 39	304	21	0.4	74	6	118210	118210
232	21.4	0.4	97	6	A77687	A77687 Sequence 39	305	21	0.4	77	8	APH505663	APH505663
233	21.4	0.4	98	6	I91508	I91508 Sequence 42	306	21	0.4	78	6	103641	103641
234	21.4	0.4	99	6	HSPH825	HSPH825	307	21	0.4	78	6	107834	107834
235	21.2	0.4	99	6	AX484373	AX484373 Sequence	308	21	0.4	80	6	AR77721	AR77721
236	21.2	0.4	51	6	AX162108	AX162108 Sequence	309	21	0.4	80	6	AR017752	AR017752
237	21.2	0.4	51	6	AR134229	AR134229 Sequence	310	21	0.4	80	6	AR094929	AR094929
238	21.2	0.4	54	6	AR134274	AR134274 Sequence	311	21	0.4	80	6	AR165588	AR165588
239	21.2	0.4	54	6	AR187339	AR187339 Sequence	312	21	0.4	81	9	AY083572	AY083572
240	21.2	0.4	59	3	NEMMTEAS	NEMMTEAS	313	21	0.4	81	11	G67356	G67356
241	21.2	0.4	64	6	AR160000	AR160000 Sequence	314	21	0.4	82	6	AR038755	AR038755
242	21.2	0.4	64	6	AR160001	AR160001 Sequence	315	21	0.4	82	6	AR059641	AR059641
243	21.2	0.4	65	6	AX080195	AX080195 Sequence	316	21	0.4	82	8	EC1RRN03	EC1RRN03
244	21.2	0.4	65	6	AX485021	AX485021 Sequence	317	21	0.4	82	8	NARRN03	NARRN03
245	21.2	0.4	67	3	AX485036	AX485036 Sequence	318	21	0.4	83	6	PYTRRN03	PYTRRN03
246	21.2	0.4	67	3	S52308	S52308 dpy-10 (e12	319	21	0.4	83	6	AX361504	AX361504
247	21.2	0.4	67	3	S67757	S67757 prostacycl	320	21	0.4	85	10	AY041942	AY041942
248	21.2	0.4	74	6	AX098134	AX098134 Sequence	321	21	0.4	85	9	HST814D	HST814D
249	21.2	0.4	75	6	FA65710S10	FA65710S10	322	21	0.4	85	6	AR042760	AR042760
250	21.2	0.4	76	6	AX080170	AX080170 Sequence	323	21	0.4	86	6	AR081435	AR081435
251	21.2	0.4	78	6	CBE345100	CBE345100	324	21	0.4	86	6	AR103763	AR103763
252	21.2	0.4	80	6	AX172495	AX172495 Sequence	325	21	0.4	88	8	AF001051	AF001051
253	21.2	0.4	81	6	AR030404	AR030404 Sequence	326	21	0.4	89	6	AX181695	AX181695
254	21.2	0.4	81	6	AF312866S1	AF312866 Homo sapi	327	21	0.4	89	8	AF001069	AF001069
255	21.2	0.4	86	5	AF044757	AF044757 Plynopro	328	21	0.4	90	6	AX089742	AX089742
256	21.2	0.4	86	6	AX240909	AX240909 Sequence	329	21	0.4	90	6	AX089743	AX089743
257	21.2	0.4	86	8	OPF489837	OPF489837	330	21	0.4	90	6	AX090197	AX090197
258	21.2	0.4	86	11	AF275602	AF275602 Bos tauru	331	21	0.4	90	9	AX090198	AX090198
259	21.2	0.4	87	6	AX033426	AX033426 Sequence	332	21	0.4	90	9	GORINSORFA	GORINSORFA
260	21.2	0.4	88	8	AB006094	AB006094 Actinidia	333	21	0.4	92	10	AY041796	AY041796
261	21.2	0.4	88	9	HUMICHTVMA	HUMICHTVMA	334	21	0.4	93	9	AB076748	AB076748
262	21.2	0.4	89	3	OPR81MYA3P	OPR81MYA3P	335	21	0.4	93	9	HOMELTV13	HOMELTV13
263	21.2	0.4	90	1	EVRECA3RE	EVRECA3RE	336	21	0.4	93	9	AX366494	AX366494
264	21.2	0.4	90	5	XX082794	XX082794 Xiphophorus	337	21	0.4	94	6	AF459837	AF459837
265	21.2	0.4	90	5	XX082795	XX082795 Xiphophorus	338	21	0.4	96	5	AF459838	AF459838
266	21.2	0.4	90	5	XX082798	XX082798 Xiphophorus	339	21	0.4	96	5	AF459839	AF459839
267	21.2	0.4	90	5	XX082801	XX082801 Xiphophorus	340	21	0.4	96	5	AF517938	AF517938
268	21.2	0.4	90	5	XX082805	XX082805 Xiphophorus	341	21	0.4	96	9	AY006263	AY006263
269	21.2	0.4	90	9	S4169552	S4169552	342	21	0.4	98	6	AX107888	AX107888
270	21.2	0.4	95	3	DDIACCTMIA	DDIACCTMIA	343	21	0.4	99	10	MUSCALINA4	MUSCALINA4
271	21.2	0.4	95	6	AR026961	AR026961	344	21	0.4	100	6	E01897	E01897
272	21.2	0.4	95	6	ATR243379	ATR243379 Arabidops	345	21	0.4	100	6	I09068	I09068
273	21.2	0.4	96	6	AX052995	AX052995	346	21	0.4	48	6	AX378186	AX378186
274	21.2	0.4	98	6	AL13606	AL13606 Oligonucleo	347	21	0.4	48	6	AX441070	AX441070
275	21.2	0.4	98	6	AX468159	AX468159 Sequence	348	21	0.4	49	6	HSU14062	HSU14062
276	21.2	0.4	98	6	E03008	E03008 DNA encodin	349	21	0.4	48	6	AX441075	AX441075
277	21.2	0.4	98	10	AF144397	AF144397 Mus muscu	350	21	0.4	50	6	AX199648	AX199648
278	21.2	0.4	99	8	AF324786	AF324786 P. gambiae	351	21	0.4	54	6	AR042332	AR042332
279	21.2	0.4	100	6	AG2H117	AG2H117	352	21	0.4	54	6	AX081483	AX081483
280	21.2	0.4	100	6	AA3851	AA3851 Sequence 25	353	21	0.4	58	1	AF094795	AF094795
281	21.2	0.4	100	6	AA3851	AA3851 Sequence 25	354	21	0.4	58	1	AF094795	AF094795
282	21.2	0.4	100	9	AF131338	AF131338 Homo sapi	355	21	0.4	60	8	AX092845	AX092845
283	21.2	0.4	100	9	FI93452S18	FI93452S18 Pan trogl	356	21	0.4	60	8	TORCPRSA	TORCPRSA
284	21.2	0.4	37	6	AX424969	AX424969 Sequence	357	21	0.4	63	6	AX482945	AX482945

C 358	20.8	0.4	65	6	AX484001	AX484001 Sequence	431	20.8	0.4	99	6	A08898	A08898 H. sapiens (
C 359	20.8	0.4	68	6	A91834	A91834 Sequence 3	C 432	20.8	0.4	99	6	AR166875	AR166875 Sequence
C 360	20.8	0.4	70	6	A35706	A35706 Synthetic o	C 433	20.8	0.4	99	6	AX023619	AX023619 Sequence
C 361	20.8	0.4	70	6	A35709	A35709 Synthetic o	C 434	20.8	0.4	99	6	AX099377	AX099377 Sequence
C 362	20.8	0.4	70	6	AR168954	AR168954 Sequence	C 435	20.8	0.4	99	6	AX192501	AX192501 Sequence
C 363	20.8	0.4	70	6	AR168957	AR168957 Sequence	C 436	20.8	0.4	99	6	114841	114841 Sequence
C 364	20.8	0.4	70	9	S65093809	S65103 OTC-ornithi	C 437	20.8	0.4	99	6	165495	165495 Sequence
C 365	20.8	0.4	72	6	AX344119	AX344119 Sequence	C 438	20.8	0.4	100	5	AF174524	AF174524 Bufo viri
C 366	20.8	0.4	72	6	AX344123	AX344123 Sequence	C 439	20.8	0.4	100	5	AF174525	AF174525 Bufo viri
C 367	20.8	0.4	73	6	AX277693	AX277693 Sequence	C 440	20.8	0.4	100	5	AF174526	AF174526 Bufo viri
C 368	20.8	0.4	76	11	AL672133	AL672133 Sequence	C 441	20.8	0.4	100	6	A76049	A76049 Sequence
C 369	20.8	0.4	78	9	AF147991	AF147991 Homo sapi	C 442	20.8	0.4	100	6	AX039309	AX039309 Sequence
C 370	20.8	0.4	78	14	AF109765	AF109765 Hepatitis	C 443	20.8	0.4	100	6	AX039518	AX039518 Sequence
C 371	20.8	0.4	79	6	I34338	I34338 Sequence 37	C 444	20.8	0.4	100	6	I17436	I17436 Sequence
C 372	20.8	0.4	80	6	AX172504	AX172504 Sequence	C 445	20.8	0.4	100	6	BD002609	BD002609 Gene comp
C 373	20.8	0.4	80	6	E03129	E03129 cDNA encodi	C 446	20.6	0.4	51	6	AX162674	AX162674 Sequence
C 374	20.8	0.4	80	9	AF088685	AF088685 Homo sapi	C 447	20.6	0.4	51	6	AX162465	AX162465 Sequence
C 375	20.8	0.4	81	6	I40754	I40754 Sequence 85	C 448	20.6	0.4	51	6	AX165725	AX165725 Sequence
C 376	20.8	0.4	81	14	AF166789	AF166789 Hepatitis	C 449	20.6	0.4	51	6	E22365	E22365 DNA encodin
C 377	20.8	0.4	83	6	AX241021	AX241021 Sequence	C 450	20.6	0.4	62	10	AF357380	AF357380 Mus muscu
C 378	20.8	0.4	83	6	AX435957	AX435957 Sequence	C 451	20.6	0.4	65	6	AX485064	AX485064 Sequence
C 379	20.8	0.4	83	6	I36506	I36506 Sequence 5	C 452	20.6	0.4	65	6	AX485219	AX485219 Sequence
C 380	20.8	0.4	83	6	168832	168832 Sequence 93	C 453	20.6	0.4	65	6	AX485346	AX485346 Sequence
C 381	20.8	0.4	84	6	AR014622	AR014622 Sequence	C 454	20.6	0.4	65	6	AX485442	AX485442 Sequence
C 382	20.8	0.4	84	6	AR014623	AR014623 Sequence	C 455	20.6	0.4	65	6	AX485489	AX485489 Sequence
C 383	20.8	0.4	84	6	AX435976	AX435976 Sequence	C 456	20.6	0.4	65	6	AR009022	AR009022 Sequence
C 384	20.8	0.4	84	6	BD010414	BD010414 ChimERIC	C 457	20.6	0.4	65	6	AR034523	AR034523 Sequence
C 385	20.8	0.4	84	6	BD010415	BD010415 ChimERIC	C 458	20.6	0.4	65	6	AR048623	AR048623 Sequence
C 386	20.8	0.4	84	6	I26759	I26759 Sequence 88	C 459	20.6	0.4	65	6	AR052677	AR052677 Sequence
C 387	20.8	0.4	84	6	I26759	I26759 Sequence 89	C 460	20.6	0.4	65	6	AR060988	AR060988 Sequence
C 388	20.8	0.4	84	6	ATH505735	ATH505735 Arabidops	C 461	20.6	0.4	65	6	AR087719	AR087719 Sequence
C 389	20.8	0.4	84	14	HIV1P74V4R	HIV1P74V4R	C 462	20.6	0.4	65	6	AR175110	AR175110 Sequence
C 390	20.8	0.4	85	6	AX099459	AX099459 Sequence	C 463	20.6	0.4	65	6	I74696	I74696 Sequence
C 391	20.8	0.4	85	6	AX436009	AX436009 Sequence	C 464	20.6	0.4	65	6	AX164004	AX164004 Sequence
C 392	20.8	0.4	86	6	AX203294	AX203294 Sequence	C 465	20.6	0.4	65	6	YSCG112	YSCG112 Sequence
C 393	20.8	0.4	86	6	AX435997	AX435997 Sequence	C 466	20.6	0.4	65	6	AR043972	AR043972 Sequence
C 394	20.8	0.4	86	6	AX436010	AX436010 Sequence	C 467	20.6	0.4	65	6	AR073505	AR073505 Sequence
C 395	20.8	0.4	86	14	HIVPOLAG	HIVPOLAG	C 468	20.6	0.4	65	6	AR103035	AR103035 Sequence
C 396	20.8	0.4	87	14	AX179367	AX179367 Sequence	C 469	20.6	0.4	65	6	AX022115	AX022115 Sequence
C 397	20.8	0.4	87	14	HIVPOLAH	HIVPOLAH	C 470	20.6	0.4	65	6	BD009385	BD009385 Sequence
C 398	20.8	0.4	89	6	A75439	A75439 Sequence 11	C 471	20.6	0.4	65	6	I93376	I93376 Sequence
C 399	20.8	0.4	89	6	A78418	A78418 Sequence 11	C 472	20.6	0.4	65	6	SLSTEL47	SLSTEL47 Sequence
C 400	20.8	0.4	89	6	AX094087	AX094087 Sequence	C 473	20.6	0.4	65	6	AR017763	AR017763 Sequence
C 401	20.8	0.4	90	1	STABLAZA	STABLAZA	C 474	20.6	0.4	65	6	AR094940	AR094940 Sequence
C 402	20.8	0.4	90	6	AR077647	AR077647 Sequence	C 475	20.6	0.4	65	6	AR165599	AR165599 Sequence
C 403	20.8	0.4	90	6	AX322428	AX322428 Sequence	C 476	20.6	0.4	65	6	AR212496	AR212496 Sequence
C 404	20.8	0.4	90	9	HUMICMFA	HUMICMFA	C 477	20.6	0.4	65	6	AX027723	AX027723 Sequence
C 405	20.8	0.4	90	14	E11248280	E11248280	C 478	20.6	0.4	65	6	AX233565	AX233565 Sequence
C 406	20.8	0.4	91	3	AF166145	AF166145 ChimERIC	C 479	20.6	0.4	65	6	119262	119262 Sequence
C 407	20.8	0.4	91	4	BTU19470	BTU19470 Bos taurus	C 480	20.6	0.4	65	6	AGLAC2E	AGLAC2E Sequence
C 408	20.8	0.4	91	4	CHU19477	CHU19477 Bos taurus	C 481	20.6	0.4	65	6	MRKIC16	MRKIC16 Sequence
C 409	20.8	0.4	92	14	HIVPOLAE	HIVPOLAE	C 482	20.6	0.4	65	6	AR042801	AR042801 Sequence
C 410	20.8	0.4	93	6	AX187688	AX187688 Human immu	C 483	20.6	0.4	65	6	AX023592	AX023592 Sequence
C 411	20.8	0.4	95	6	BD003045	BD003045 Sequence	C 484	20.6	0.4	65	6	MMGXAD33	MMGXAD33 Sequence
C 412	20.8	0.4	95	11	G12071	G12071 Design, c	C 485	20.6	0.4	65	6	AR007076	AR007076 Sequence
C 413	20.8	0.4	96	11	HSC124EH4	HSC124EH4	C 486	20.6	0.4	65	6	AR111100	AR111100 Sequence
C 414	20.8	0.4	97	3	AY009547	AY009547 Boophilus	C 487	20.6	0.4	65	6	AX167497	AX167497 Sequence
C 415	20.8	0.4	97	6	AR014605	AR014605 Sequence	C 488	20.6	0.4	65	6	I75016	I75016 Sequence
C 416	20.8	0.4	97	6	AR014607	AR014607 Sequence	C 489	20.6	0.4	65	6	AF317983	AF317983 Sequence
C 417	20.8	0.4	97	6	AR014617	AR014617 Sequence	C 490	20.6	0.4	65	6	AF001066	AF001066 Sequence
C 418	20.8	0.4	97	6	AR014621	AR014621 Sequence	C 491	20.6	0.4	65	6	AF001067	AF001067 Sequence
C 419	20.8	0.4	97	6	AR094798	AR094798 Sequence	C 492	20.6	0.4	65	6		
C 420	20.8	0.4	97	6	BD010397	BD010397 ChimERIC	C 493	20.6	0.4	65	6		
C 421	20.8	0.4	97	6	AR165457	AR165457 Sequence	C 494	20.6	0.4	65	6		
C 422	20.8	0.4	97	6	BD010397	BD010397 ChimERIC	C 495	20.6	0.4	65	6		
C 423	20.8	0.4	97	6	BD010409	BD010409 ChimERIC	C 496	20.6	0.4	65	6		
C 424	20.8	0.4	97	6	I26746	I26746 Sequence 38	C 497	20.6	0.4	65	6		
C 425	20.8	0.4	97	6	I26748	I26748 Sequence 42	C 498	20.6	0.4	65	6		
C 426	20.8	0.4	98	6	AX039308	AX039308 Sequence	C 499	20.6	0.4	65	6		
C 427	20.8	0.4	98	6	AX039517	AX039517 Sequence	C 500	20.6	0.4	65	6		
C 428	20.8	0.4	98	6	E26102	E26102 Novel DNA f	C 501	20.6	0.4	65	6		
C 429	20.8	0.4	98	6	MMV81N28	MMV81N28	C 502	20.6	0.4	65	6		
C 430	20.8	0.4	98	10			C 503	20.6	0.4	65	6		

C 504	20.6	0.4	89	8	AF001068	AF001068 Gigaaspora
C 505	20.6	0.4	89	9	HS4230050	AA2330050 Homo sapi
C 506	20.6	0.4	90	6	AX451463	AX451463 Sequence
C 507	20.6	0.4	90	10	MUSIGRW2	M00548 mouse lg ka
C 508	20.6	0.4	90	12	SYNDEL341	M10684 X.laevius DN
C 509	20.6	0.4	90	17	HS2EC0317	X85354 H.sapiens t
C 510	20.6	0.4	91	6	AR072979	AR072979 Sequence
C 511	20.6	0.4	91	10	MUSALC2B11	M95510 Mus musculus
C 512	20.6	0.4	92	9	HUMMCA04	M14424 Human mediu
C 513	20.6	0.4	94	6	AX366494	AX366494 Sequence
C 514	20.6	0.4	96	6	AA4582	AA4582 Sequence 18
C 515	20.6	0.4	96	10	RATRADC10	L32996 Rat aromati
C 516	20.6	0.4	96	11	G16140	G16140 SMS2675 Br
C 517	20.6	0.4	97	11	AF247507	AF247507 Strongylo
C 518	20.6	0.4	97	11	AL773278	AL773278 Arabidops
C 519	20.6	0.4	97	11	AL773280	AL773280 Arabidops
C 520	20.6	0.4	97	11	AL773283	AL773283 Arabidops
C 521	20.6	0.4	97	11	AL773286	AL773286 Arabidops
C 522	20.6	0.4	98	6	AX192825	AX192825 Sequence
C 523	20.6	0.4	100	6	AA3830	AA3830 Sequence 4
C 524	20.6	0.4	100	6	AA3845	AA3845 Sequence 19
C 525	20.6	0.4	100	6	IL17407	IL17407 Sequence 4
C 526	20.6	0.4	100	6	IL17422	IL17422 Sequence 19
C 527	20.6	0.4	100	8	AF062779	AF062779 Glycine m
C 528	20.6	0.4	100	9	AJ08118	AJ08118 Homo sapi
C 529	20.6	0.4	100	14	POL3BRA	P00263 Human polio
C 530	20.6	0.4	40	6	AA5366	AA5366 Sequence 2
C 531	20.4	0.4	45	6	AX490814	AX490814 Sequence
C 532	20.4	0.4	51	6	AX158827	AX158827 Sequence
C 533	20.4	0.4	51	6	AX163076	AX163076 Sequence
C 534	20.4	0.4	57	6	AX37072	AX37072 Sequence 15
C 535	20.4	0.4	57	6	E15476	E15476 Primer 7/11
C 536	20.4	0.4	57	6	E15476	E15476 Primer 7/11
C 537	20.4	0.4	59	6	AX341922	AX341922 Sequence
C 538	20.4	0.4	60	6	AX139536	AX139536 Sequence
C 539	20.4	0.4	62	6	AX484256	AX484256 Sequence
C 540	20.4	0.4	65	6	AX485005	AX485005 Sequence
C 541	20.4	0.4	65	6	AX485830	AX485830 Sequence
C 542	20.4	0.4	65	6	AX485885	AX485885 Sequence
C 543	20.4	0.4	68	14	MHU19937	U19937 Mouse hepat
C 544	20.4	0.4	69	6	I16689	I16689 Sequence 29
C 545	20.4	0.4	69	6	I16942	I16942 Sequence 29
C 546	20.4	0.4	69	11	G38355	G38355 ST638 Misc
C 547	20.4	0.4	71	6	E34286	E34286 Environment
C 548	20.4	0.4	71	6	E34286	E34286 Environment
C 549	20.4	0.4	72	8	PE2240490	PE2240490 Physconia
C 550	20.4	0.4	73	6	AI9088	AI9088 Nucleotide
C 551	20.4	0.4	73	6	AI9088	AI9088 Nucleotide
C 552	20.4	0.4	74	6	AI9088	AI9088 Nucleotide
C 553	20.4	0.4	74	6	AI9088	AI9088 Nucleotide
C 554	20.4	0.4	75	1	SAU73399	SAU73399 Saccharom
C 555	20.4	0.4	75	3	AX107615	AX107615 Adineta v
C 556	20.4	0.4	75	6	AX107661	AX107661 Sequence
C 557	20.4	0.4	75	9	S70579	S70579 Homo sapien
C 558	20.4	0.4	76	6	AR042692	AR042692 Sequence
C 559	20.4	0.4	76	6	AR064825	AR064825 Sequence
C 560	20.4	0.4	76	6	AR125951	AR125951 Sequence
C 561	20.4	0.4	76	6	AX028738	AX028738 Sequence
C 562	20.4	0.4	76	6	I47271	I47271 Sequence 20
C 563	20.4	0.4	77	8	MISC41	X00892 Yeast mtoc
C 564	20.4	0.4	77	8	MISC41	X00892 Yeast mtoc
C 565	20.4	0.4	78	3	AY013952	AY013952 Eupriat
C 566	20.4	0.4	78	3	AY013958	AY013958 Habrotr
C 567	20.4	0.4	78	3	AY014000	AY014000 Habrotr
C 568	20.4	0.4	78	10	MUSCAXA	M37591 Mouse T cel
C 569	20.4	0.4	79	6	AX164120	AX164120 Sequence
C 570	20.4	0.4	80	5	AF117288	AF117288 Gallus ga
C 571	20.4	0.4	80	5	AF117288	AF117288 Gallus ga
C 572	20.4	0.4	81	14	AF155884	AF155884 HIV-1 iso
C 573	20.4	0.4	81	14	AF221297	AF221297 Hepatit
C 574	20.4	0.4	81	14	AF221297	AF221297 Hepatit
C 575	20.4	0.4	81	14	AF221297	AF221297 Hepatit
C 576	20.4	0.4	81	14	NT087652	NT087652 Notwilk 11k
C 577	20.4	0.4	82	11	HUMSWX1168	I42656 Human chrom
C 578	20.4	0.4	83	6	E02071	E02071 RNA encodin
C 579	20.4	0.4	85	3	DROTKO10	L00363 D.melanog
C 580	20.4	0.4	85	6	AA5374	AA5374 Sequence 44
C 581	20.4	0.4	85	6	AR061179	AR061179 Sequence
C 582	20.4	0.4	85	9	HSWG3B103	X86915 H.sapiens s
C 583	20.4	0.4	85	11	HUMSWX2039	L41114 Human chrom
C 584	20.4	0.4	86	10	AY042056	AY042056 Sigmodon
C 585	20.4	0.4	86	10	AY042056	AY042056 Sigmodon
C 586	20.4	0.4	88	11	MUSIGHCL	AF001073 Scutell
C 587	20.4	0.4	88	11	HUMSWX1287	AF001073 Scutell
C 588	20.4	0.4	88	11	HUMSWX1287	AF001073 Scutell
C 589	20.4	0.4	89	6	AR204023	AR204023 Sequence
C 590	20.4	0.4	89	6	AR204023	AR204023 Sequence
C 591	20.4	0.4	89	10	MMSNOR35	Z69625 M.musculus
C 592	20.4	0.4	89	14	E11248270	AJ248270 Echovirus
C 593	20.4	0.4	89	14	E11248272	AJ248272 Echovirus
C 594	20.4	0.4	90	14	E11248275	AJ248275 Echovirus
C 595	20.4	0.4	90	14	E11248279	AJ248279 Echovirus
C 596	20.4	0.4	91	6	I02847	I02847 Sequence 3
C 597	20.4	0.4	91	6	I03202	I03202 Sequence 3
C 598	20.4	0.4	91	6	AF318002	AF318002 Arabidops
C 599	20.4	0.4	91	8	AF318003	AF318003 Arabidops
C 600	20.4	0.4	91	9	AF321383S1	AF321383 Callithr
C 601	20.4	0.4	91	14	E11248274	AJ248274 Echovirus
C 602	20.4	0.4	92	5	AF420513	AF420513 Salmo sal
C 603	20.4	0.4	92	6	AX023584	AX023584 Sequence
C 604	20.4	0.4	92	6	AX039519	AX039519 Sequence
C 605	20.4	0.4	92	6	AX039519	AX039519 Sequence
C 606	20.4	0.4	93	6	AX106439	AX106439 Sequence
C 607	20.4	0.4	93	6	AX140730	AX140730 Sequence
C 608	20.4	0.4	93	6	AX200590	AX200590 Sequence
C 609	20.4	0.4	93	6	AX267246	AX267246 Sequence
C 610	20.4	0.4	93	14	HIVPOLAP	M64028 Human immun
C 611	20.4	0.4	94	6	AX039311	AX039311 Sequence
C 612	20.4	0.4	94	14	E11248281	AJ248281 Echovirus
C 613	20.4	0.4	95	14	IBDVUTR5	AF479592 Zeta may
C 614	20.4	0.4	95	14	IBDVUTR5	AF479592 Zeta may
C 615	20.4	0.4	95	14	IBDVUTR9	X84026 Infectious
C 616	20.4	0.4	96	1	S57038	S57038 Infectious
C 617	20.4	0.4	96	9	HUMDHL.P03	S57038 Infectious
C 618	20.4	0.4	96	9	S79729	S79729 glycoprotein
C 619	20.4	0.4	96	14	HIVU108292	U28292 Human immun
C 620	20.4	0.4	96	14	HIVU108292	U28292 Human immun
C 621	20.4	0.4	97	6	ASP6301	AJ006301 Phocoea
C 622	20.4	0.4	97	6	ASP6301	AJ006301 Phocoea
C 623	20.4	0.4	98	9	HUMSPRC14	AJ21012 PTH for the
C 624	20.4	0.4	98	9	HUMSPRC14	AJ21012 PTH for the
C 625	20.4	0.4	98	9	GA2691	GA2691 Human putat
C 626	20.4	0.4	98	9	GA2691	GA2691 Human putat
C 627	20.4	0.4	99	9	AB044101	AB044101 Homo sapi
C 628	20.4	0.4	99	10	HSADHSC09	AB044101 Homo sapi
C 629	20.4	0.4	99	10	HSADHSC09	AB044101 Homo sapi
C 630	20.4	0.4	99	10	HSADHSC09	AB044101 Homo sapi
C 631	20.4	0.4	100	11	HUMDUT1990A	X89689 R.tattus (S
C 632	20.4	0.4	100	11	HUMDUT1990A	X89689 R.tattus (S
C 633	20.4	0.4	100	14	HIVU045229	L30648 Human STS D
C 634	20.4	0.4	100	14	HIVU045231	U45229 Human immun
C 635	20.4	0.4	100	14	HIVU045233	U45229 Human immun
C 636	20.4	0.4	100	14	HIVU045233	U45229 Human immun
C 637	20.4	0.4	100	14	HIVU045512	U45512 Human immun
C 638	20.4	0.4	100	14	HIVU045512	U45512 Human immun
C 639	20.4	0.4	100	14	HIVU045514	U45514 Human immun
C 640	20.4	0.4	100	14	HIVU045516	U45516 Human immun
C 641	20.4	0.4	100	14	HIVU045560	U45560 Human immun
C 642	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 643	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 644	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 645	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 646	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 647	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 648	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 649	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 650	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 651	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 652	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 653	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 654	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 655	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 656	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 657	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 658	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 659	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 660	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 661	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 662	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 663	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 664	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 665	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 666	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 667	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 668	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 669	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 670	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 671	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 672	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 673	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 674	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 675	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 676	20.4	0.4	100	14	HIVU045568	U45568 Human immun
C 677	20.4	0.4	100	14	HIVU045568	U45568

C 650	20.2	0.4	51	6	AX116841	Sequence	723	20.2	0.4	96	10	RATPRO05
C 651	20.2	0.4	51	6	AX163176	Sequence	C 724	20.2	0.4	96	11	HS186XG7
C 652	20.2	0.4	51	6	AX165692	Sequence	725	20.2	0.4	97	8	S52653
C 653	20.2	0.4	60	6	AR0179559	Sequence	726	20.2	0.4	98	6	AR081710
C 654	20.2	0.4	63	6	AR031249	Sequence	727	20.2	0.4	98	6	E36069
C 655	20.2	0.4	63	6	AR075297	Sequence	728	20.2	0.4	98	6	I49625
C 656	20.2	0.4	63	6	AR099956	Sequence	729	20.2	0.4	98	6	I71467
C 657	20.2	0.4	63	6	AR169261	Sequence	730	20.2	0.4	99	3	AF343561
C 658	20.2	0.4	63	6	AR183595	Sequence	731	20.2	0.4	99	3	HSPETS1
C 659	20.2	0.4	63	9	AF189477	Homo sapi	732	20.2	0.4	99	8	AF318055
C 660	20.2	0.4	65	6	AX484349	Sequence	733	20.2	0.4	99	8	S52652
C 661	20.2	0.4	65	6	AX485855	Sequence	734	20.2	0.4	99	9	AF005957
C 662	20.2	0.4	65	6	AX485925	Sequence	735	20.2	0.4	99	14	PCSVS15
C 663	20.2	0.4	65	6	AX485926	Sequence	C 736	20.2	0.4	99	14	PCSVS15A
C 664	20.2	0.4	65	6	AX486115	Sequence	737	20.2	0.4	100	1	ECOTNDCA
C 665	20.2	0.4	65	10	MUSPCKGPEC	104516 Mus musculu	C 738	20.2	0.4	100	6	AX379183
C 666	20.2	0.4	66	9	HSU91195	U91195 Homo sapien	C 739	20.2	0.4	100	11	AL807535
C 667	20.2	0.4	67	3	AF177249	AR077249 Bodo salt	C 740	20.2	0.4	100	11	G32918
C 668	20.2	0.4	69	6	AR007248	Sequence	741	20.2	0.4	100	11	HUMSXA149
C 669	20.2	0.4	69	6	AR012463	Sequence	742	20.2	0.4	38	6	AR194938
C 670	20.2	0.4	69	6	AR020291	Sequence	743	20.2	0.4	38	6	BD006438
C 671	20.2	0.4	69	6	AR062452	Sequence	744	20.2	0.4	38	6	BD006558
C 672	20.2	0.4	69	6	AR109312	Sequence	745	20.2	0.4	40	6	AR142030
C 673	20.2	0.4	69	6	AR170034	Sequence	746	20.2	0.4	40	6	I59897
C 674	20.2	0.4	69	6	AR170034	Sequence	747	20.2	0.4	40	6	I68066
C 675	20.2	0.4	69	6	AX193362	Sequence	748	20.2	0.4	40	6	I68755
C 676	20.2	0.4	69	6	I27738	Sequence	749	20.2	0.4	40	6	I68755
C 677	20.2	0.4	69	6	I82637	Sequence	750	20.2	0.4	41	6	I57880
C 678	20.2	0.4	71	6	AR007247	Sequence	C 751	20.2	0.4	41	6	AR009854
C 679	20.2	0.4	71	6	AR062451	Sequence	C 752	20.2	0.4	45	6	AL17057
C 680	20.2	0.4	71	6	AR170033	Sequence	C 753	20.2	0.4	45	6	AR014432
C 681	20.2	0.4	71	6	AR170460	Sequence	C 754	20.2	0.4	45	6	IL1875
C 682	20.2	0.4	71	6	I27737	Sequence	C 755	20.2	0.4	47	6	AX378294
C 683	20.2	0.4	72	8	NEUMTGA	101248 N. crassa ml	C 756	20.2	0.4	48	6	AR032581
C 684	20.2	0.4	73	6	AL9092	AL9092 Nucleotide	C 757	20.2	0.4	48	6	AR209245
C 685	20.2	0.4	74	6	AL9091	K00144 Neurospora	C 758	20.2	0.4	48	6	I29321
C 686	20.2	0.4	75	8	NEUMTGA	AF043843 Homo sapi	C 759	20.2	0.4	48	6	I90995
C 687	20.2	0.4	75	9	AF043843	AF043844 Homo sapi	C 760	20.2	0.4	50	6	AX162066
C 688	20.2	0.4	75	9	AF043844	Sequence	C 761	20.2	0.4	51	6	AX156866
C 689	20.2	0.4	76	5	S67412	S67414 Xenopus lae	C 762	20.2	0.4	51	6	AX158150
C 690	20.2	0.4	76	5	S67414	S67416 Physalis	C 763	20.2	0.4	51	6	AX160456
C 691	20.2	0.4	78	8	AF374443	S67416 Silurana tr	C 764	20.2	0.4	51	6	AX160667
C 692	20.2	0.4	79	5	S67416	S67415 Xenopus lae	C 765	20.2	0.4	51	6	AX160928
C 693	20.2	0.4	80	5	S67415	AF327690 Homo sapi	C 766	20.2	0.4	51	6	AX161269
C 694	20.2	0.4	81	9	F327658S33	L77117 Homo sapien	C 767	20.2	0.4	51	6	AX199320
C 695	20.2	0.4	81	9	F327658S33	M19124 Human sapien	C 768	20.2	0.4	51	6	AX199320
C 696	20.2	0.4	82	9	HUMTCHBD	AX240981 Sequence	C 769	20.2	0.4	51	6	AX203978
C 697	20.2	0.4	83	6	AX240981	AF37454 Mus muscu	C 770	20.2	0.4	51	6	AX203978
C 698	20.2	0.4	83	10	AF37454	AR014627 Sequence	C 771	20.2	0.4	54	6	AR081883
C 699	20.2	0.4	84	6	AR014627	BD010419 Chimeric	C 772	20.2	0.4	54	6	AR159917
C 700	20.2	0.4	84	6	BD010419	I26742 Sequence	C 773	20.2	0.4	55	14	HIVU45027
C 701	20.2	0.4	84	6	I26742	AX078800 Sequence	C 774	20.2	0.4	55	14	HIVU45047
C 702	20.2	0.4	86	6	AX078800	AY112767 Sus scrofa	C 775	20.2	0.4	55	14	HIVU45047
C 703	20.2	0.4	87	4	AX112767	AR055088 Sequence	C 776	20.2	0.4	55	14	HIVU45049
C 704	20.2	0.4	87	6	AR055088	AR156337 Sequence	C 777	20.2	0.4	55	14	HIVU45051
C 705	20.2	0.4	87	6	AR156337	M63172 O. falax 81	C 778	20.2	0.4	55	14	HIVU45057
C 706	20.2	0.4	89	5	RCSCRNA	Z11765 R. catesbeia	C 779	20.2	0.4	55	14	HIVU45069
C 707	20.2	0.4	89	5	OFABMVB3P	U82796 Xiphophorus	C 780	20.2	0.4	55	14	HIVU45071
C 708	20.2	0.4	90	5	XX082796	AR072980 Sequence	C 781	20.2	0.4	55	14	HIVU45073
C 709	20.2	0.4	90	6	AR072980	X68760 H. sapiens K	C 782	20.2	0.4	55	14	HIVU45075
C 710	20.2	0.4	92	9	HSRLX11A	AR119476 Sequence	C 783	20.2	0.4	55	14	HIVU45077
C 711	20.2	0.4	95	6	AR119476	AR119476 Sequence	C 784	20.2	0.4	55	14	HIVU45079
C 712	20.2	0.4	95	6	AR150837	AR150837 Sequence	C 785	20.2	0.4	55	14	HIVU45079
C 713	20.2	0.4	95	6	AR150837	I65715 Sequence	C 786	20.2	0.4	55	14	HIVU45079
C 714	20.2	0.4	95	6	I65715	I65715 Sequence	C 787	20.2	0.4	55	14	HIVU45079
C 715	20.2	0.4	95	6	I65715	I65715 Sequence	C 788	20.2	0.4	55	14	HIVU45079
C 716	20.2	0.4	95	6	I65715	I65715 Sequence	C 789	20.2	0.4	55	14	HIVU45079
C 717	20.2	0.4	95	6	I65715	I65715 Sequence	C 790	20.2	0.4	55	14	HIVU45079
C 718	20.2	0.4	95	10	MMVSIN27	U29110 Human leiom	C 791	20.2	0.4	55	14	HIVU45087
C 719	20.2	0.4	96	1	ECOC625	Z12485 M. musculus	C 792	20.2	0.4	55	14	HIVU45091
C 720	20.2	0.4	96	9	AY006145	M10419 E. coli heat	C 793	20.2	0.4	55	14	HIVU45093
C 721	20.2	0.4	96	9	AY006145	AY006145 Homo sapi	C 794	20.2	0.4	56	6	AX358702
C 722	20.2	0.4	96	9	S45135	S45135 APP-amyloid	C 795	20.2	0.4	58	9	HUMBLISC
					S45136	APP-amyloid						

C 796	20	0.4	59	6	AX358709	AX358709 Sequence	869	20	0.4	91	4	BMU19471	U19471 Bos taurus
C 797	20	0.4	59	6	AX358710	AX358710 Sequence	C 870	20	0.4	91	6	AX244617	AX244617 Sequence
C 798	20	0.4	59	6	AX358715	AX358715 Sequence	C 871	20	0.4	91	6	AX244617	AX244617 Sequence
C 799	20	0.4	59	6	AX358716	AX358716 Sequence	C 872	20	0.4	92	6	E05823	E05823 DNA encodin
C 800	20	0.4	60	6	AR068207	AR068207 Sequence	C 873	20	0.4	93	5	XMO82800	XMO82800 Xiphophorus
C 801	20	0.4	60	6	AR076959	AR076959 Sequence	C 874	20	0.4	93	6	AR174921	AR174921 Sequence
C 802	20	0.4	60	6	AR078792	AR078792 Sequence	C 875	20	0.4	93	6	AX084756	AX084756 Sequence
C 803	20	0.4	61	6	AR078792	AR078792 Sequence	C 876	20	0.4	93	6	AX282691	AX282691 Sequence
C 804	20	0.4	61	6	AR138413	AR138413 Sequence	C 877	20	0.4	93	6	HSRNP2509	HSRNP2509 Human renal
C 805	20	0.4	62	6	AR1371	AR1371 Repeat nucl	C 878	20	0.4	93	10	MMU26249	MMU26249 Mus musculus
C 806	20	0.4	63	6	AX037305	AX037305 Sequence	C 879	20	0.4	94	5	AF044762	AF044762 Physalosoma
C 807	20	0.4	64	6	AX482832	AX482832 Sequence	C 880	20	0.4	94	6	AR205582	AR205582 Sequence
C 808	20	0.4	65	6	AX484244	AX484244 Sequence	C 881	20	0.4	94	6	AX076600	AX076600 Sequence
C 809	20	0.4	65	6	AX484729	AX484729 Sequence	C 882	20	0.4	95	3	LEIKPMRFA	LEIKPMRFA L. tarentola
C 810	20	0.4	65	6	AX485562	AX485562 Sequence	C 883	20	0.4	95	6	AR041085	AR041085 Sequence
C 811	20	0.4	65	6	AX486142	AX486142 Sequence	C 884	20	0.4	95	6	AR050589	AR050589 Sequence
C 812	20	0.4	65	6	AX396584	AX396584 Sequence	C 885	20	0.4	95	6	AR060693	AR060693 Sequence
C 813	20	0.4	67	6	AX365620	AX365620 Sequence	C 886	20	0.4	95	6	AR063126	AR063126 Sequence
C 814	20	0.4	67	6	AX365620	AX365620 Sequence	C 887	20	0.4	95	6	AR117015	AR117015 Sequence
C 815	20	0.4	68	6	AX365620	AX365620 Sequence	C 888	20	0.4	95	6	HSRNP2509	HSRNP2509 Human renal
C 816	20	0.4	68	6	AX365620	AX365620 Sequence	C 889	20	0.4	95	6	HSRNP2509	HSRNP2509 Human renal
C 817	20	0.4	68	6	AX365620	AX365620 Sequence	C 890	20	0.4	95	6	HSRNP2509	HSRNP2509 Human renal
C 818	20	0.4	70	6	AR207718	AR207718 Sequence	C 891	20	0.4	96	3	AF411999	AF411999 Formica
C 819	20	0.4	70	6	AR207718	AR207718 Sequence	C 892	20	0.4	96	3	AX039237	AX039237 Sequence
C 820	20	0.4	72	8	CRMTTTRNA	CRMTTTRNA Sequence	C 893	20	0.4	96	6	AX039238	AX039238 Sequence
C 821	20	0.4	73	5	AF301558	AF301558 Bucephala	C 894	20	0.4	96	6	AX039477	AX039477 Sequence
C 822	20	0.4	73	6	AR091365	AR091365 Sequence	C 895	20	0.4	96	6	AX039478	AX039478 Sequence
C 823	20	0.4	74	6	AR63124	AR63124 Sequence	C 896	20	0.4	96	6	AX134835	AX134835 Sequence
C 824	20	0.4	74	6	AR134559	AR134559 Sequence	C 897	20	0.4	96	6	AX134836	AX134836 Sequence
C 825	20	0.4	74	6	AR233515	AR233515 Sequence	C 898	20	0.4	96	6	AX134925	AX134925 Sequence
C 826	20	0.4	75	9	AR043921	AR043921 Sequence	C 899	20	0.4	96	6	AX135043	AX135043 Sequence
C 827	20	0.4	75	9	HSLS90	HSLS90 Sequence	C 900	20	0.4	96	6	AX135044	AX135044 Sequence
C 828	20	0.4	76	9	HSLS90	HSLS90 Sequence	C 901	20	0.4	96	6	AX363260	AX363260 Sequence
C 829	20	0.4	76	9	AX233554	AX233554 Sequence	C 902	20	0.4	96	6	AR06143510	AR06143510 Sequence
C 830	20	0.4	80	6	E02438	E02438 DNA encodin	C 903	20	0.4	98	3	AF263206	AF263206 Sequence
C 831	20	0.4	80	6	E02442	E02442 DNA encodin	C 904	20	0.4	98	6	AX210035	AX210035 Sequence
C 832	20	0.4	80	6	E02502	E02502 DNA encodin	C 905	20	0.4	99	6	AS0274	AS0274 Sequence
C 833	20	0.4	81	6	AR062736	AR062736 Sequence	C 906	20	0.4	100	6	HSWC27604	HSWC27604 Sequence
C 834	20	0.4	81	6	PTTRG	PTTRG Sequence	C 907	20	0.4	100	6	AR69876	AR69876 Sequence
C 835	20	0.4	82	6	AR051511	AR051511 Sequence	C 908	20	0.4	100	6	AX12897	AX12897 Sequence
C 836	20	0.4	82	6	AR072651	AR072651 Sequence	C 909	20	0.4	100	6	AX260734	AX260734 Sequence
C 837	20	0.4	82	6	AR073196	AR073196 Sequence	C 910	20	0.4	100	6	HUMIGJHC	HUMIGJHC Human ig ge
C 838	20	0.4	82	6	AR051521	AR051521 Sequence	C 911	20	0.4	100	6	AX383987	AX383987 Sequence
C 839	20	0.4	82	6	AR051521	AR051521 Sequence	C 912	20	0.4	100	6	AX015104	AX015104 Sequence
C 840	20	0.4	84	6	AR072661	AR072661 Sequence	C 913	20	0.4	100	6	AX160356	AX160356 Sequence
C 841	20	0.4	84	6	AR072661	AR072661 Sequence	C 914	20	0.4	100	6	AX485736	AX485736 Sequence
C 842	20	0.4	84	6	MMU03439	MMU03439 M. musculu	C 915	20	0.4	100	6	E59807	E59807 Method for
C 843	20	0.4	84	10	MUSTGKCP	MUSTGKCP Mouse activ	C 916	20	0.4	100	6	AX117265	AX117265 Sequence
C 844	20	0.4	84	10	MUSTGKCP	MUSTGKCP Mouse activ	C 917	20	0.4	100	6	AX158178	AX158178 Sequence
C 845	20	0.4	84	10	MUSTGKCP	MUSTGKCP Mouse activ	C 918	20	0.4	100	6	AX158178	AX158178 Sequence
C 846	20	0.4	85	3	AF318494	AF318494 Scutiger	C 919	20	0.4	100	6	AX158178	AX158178 Sequence
C 847	20	0.4	85	3	AF318494	AF318494 Scutiger	C 920	20	0.4	100	6	AX158178	AX158178 Sequence
C 848	20	0.4	87	6	AX241048	AX241048 Homo sapi	C 921	20	0.4	100	6	AX482193	AX482193 Sequence
C 849	20	0.4	87	6	HSXARRES01	HSXARRES01 Homo sapi	C 922	20	0.4	100	6	CCR61J2	CCR61J2 Sequence
C 850	20	0.4	87	10	MUSIGHNE	MUSIGHNE Mouse activ	C 923	20	0.4	100	6	AF040200	AF040200 Homo sapi
C 851	20	0.4	88	1	HEA620	HEA620 H. influenza	C 924	20	0.4	100	6	AF040200	AF040200 Homo sapi
C 852	20	0.4	88	1	HEA620	HEA620 H. influenza	C 925	20	0.4	100	6	AF040200	AF040200 Homo sapi
C 853	20	0.4	88	6	AX465615	AX465615 Sequence	C 926	20	0.4	100	6	AX465615	AX465615 Sequence
C 854	20	0.4	88	6	HSILGRF26	HSILGRF26 Homo sapi	C 927	20	0.4	100	6	AR121381	AR121381 Sequence
C 855	20	0.4	88	6	AR045023	AR045023 Sequence	C 928	20	0.4	100	6	AR121381	AR121381 Sequence
C 856	20	0.4	89	6	IL8555	IL8555 Sequence	C 929	20	0.4	100	6	AX022595	AX022595 Sequence
C 857	20	0.4	89	6	IL8555	IL8555 Sequence	C 930	20	0.4	100	6	AX022595	AX022595 Sequence
C 858	20	0.4	89	6	IL8555	IL8555 Sequence	C 931	20	0.4	100	6	AX022595	AX022595 Sequence
C 859	20	0.4	89	6	IL8555	IL8555 Sequence	C 932	20	0.4	100	6	AX022595	AX022595 Sequence
C 860	20	0.4	89	6	IL8555	IL8555 Sequence	C 933	20	0.4	100	6	AX022595	AX022595 Sequence
C 861	20	0.4	89	6	IL8555	IL8555 Sequence	C 934	20	0.4	100	6	AX022595	AX022595 Sequence
C 862	20	0.4	89	6	IL8555	IL8555 Sequence	C 935	20	0.4	100	6	AX022595	AX022595 Sequence
C 863	20	0.4	89	6	IL8555	IL8555 Sequence	C 936	20	0.4	100	6	AX022595	AX022595 Sequence
C 864	20	0.4	89	6	IL8555	IL8555 Sequence	C 937	20	0.4	100	6	AX022595	AX022595 Sequence
C 865	20	0.4	89	6	IL8555	IL8555 Sequence	C 938	20	0.4	100	6	AX022595	AX022595 Sequence
C 866	20	0.4	89	6	IL8555	IL8555 Sequence	C 939	20	0.4	100	6	AX022595	AX022595 Sequence
C 867	20	0.4	89	6	IL8555	IL8555 Sequence	C 940	20	0.4	100	6	AX022595	AX022595 Sequence
C 868	20	0.4	89	6	IL8555	IL8555 Sequence	C 941	20	0.4	100	6	AX022595	AX022595 Sequence

942	19.8	0.4	70	6	AX347691	AX347691 Sequence
C 943	19.8	0.4	71	6	AR140783	AR140783 Sequence
C 944	19.8	0.4	71	6	193462	193462 Sequence 60
C 945	19.8	0.4	71	6	195089	195089 Sequence 60
946	19.8	0.4	72	6	AX363480	AX363480 Sequence
947	19.8	0.4	72	10	RATCKRNP2	D11319 Rattus norv
948	19.8	0.4	72	10	SYN1718PPS	M35460 Plasmid prw
949	19.8	0.4	73	10	MM0403188	AI403188 M.musculi
C 950	19.8	0.4	74	6	A86634	A86634 Sequence 43
C 951	19.8	0.4	74	6	A86635	A86635 Sequence 44
C 952	19.8	0.4	74	6	AR118843	AR118843 Sequence 35
C 953	19.8	0.4	74	6	I06415	I06415 Sequence 4
954	19.8	0.4	75	6	A83284	A83284 Sequence 4
955	19.8	0.4	75	6	AR011553	AR011553 Sequence
C 956	19.8	0.4	75	6	AR051453	AR051453 Sequence
C 957	19.8	0.4	75	6	AR072593	AR072593 Sequence
C 958	19.8	0.4	75	6	AR073138	AR073138 Sequence
959	19.8	0.4	75	6	AX195253	AX195253 Sequence
960	19.8	0.4	75	6	AX241126	AX241126 Sequence
961	19.8	0.4	75	6	I18191	I18191 Sequence 42
962	19.8	0.4	75	14	MH019934	U19934 Mouse hepat
C 963	19.8	0.4	76	3	AF017049	AF017049 Plasmid
C 964	19.8	0.4	76	3	AY013972	AY013972 Drosophila
C 965	19.8	0.4	76	11	HUMUT628A	I30054 Human STS U
C 966	19.8	0.4	78	9	HS2421956	AJ2421956 Homo sapi
C 967	19.8	0.4	78	9	HUMTCATE	W23343 Homo sapien
C 968	19.8	0.4	79	6	AX381561	AX381561 Sequence
C 969	19.8	0.4	79	11	AL823769	AL823769 Arabidops
C 970	19.8	0.4	80	3	DROR1584	M0167 D.melanogas
C 971	19.8	0.4	80	3	DROR1586	M1539 D.melanogas
972	19.8	0.4	80	6	AX241111	AX241111 Sequence
973	19.8	0.4	80	6	AX287564	AX287564 Sequence
C 974	19.8	0.4	80	6	AX287565	AX287565 Sequence
C 975	19.8	0.4	80	6	I73619	I73619 Sequence 73
C 976	19.8	0.4	80	9	S64866S1	S64866 Hylobates s
977	19.8	0.4	81	1	BACRMAE	M15407 B.subtilis
C 978	19.8	0.4	81	9	AF043839	AF043839 Homo sapi
C 979	19.8	0.4	81	9	AF043839	AF043839 Homo sapi
C 980	19.8	0.4	81	9	HUMCD3454	M81941 Human CD34
C 981	19.8	0.4	81	14	AB089884	AB089884 Notwalk v
C 982	19.8	0.4	82	9	AF274846	AF274846 Homo sapi
C 983	19.8	0.4	82	10	RN0230619	AJ330619 Rattus no
C 984	19.8	0.4	83	6	AR042802	AR042802 Sequence
C 985	19.8	0.4	83	9	HUMFON1112	L47708 Homo sapien
986	19.8	0.4	84	6	I11718	I11718 Sequence 4
987	19.8	0.4	84	6	I11734	I11734 Sequence 4
988	19.8	0.4	84	6	I43850	I43850 Sequence 4
C 989	19.8	0.4	84	10	MUSIGRCOV	M30432 Mouse 19 um
C 990	19.8	0.4	85	6	AX025268	AX025268 Sequence
C 991	19.8	0.4	85	9	S75425806	S75436 collagen ty
C 992	19.8	0.4	86	6	AX039312	AX039312 Sequence
C 993	19.8	0.4	86	6	AX039521	AX039521 Sequence
C 994	19.8	0.4	86	6	AX240975	AX240975 Sequence
995	19.8	0.4	86	11	G68158	G68158 D7S3169 (34
996	19.8	0.4	88	6	AR043969	AR043969 Sequence
997	19.8	0.4	88	6	AR073502	AR073502 Sequence
998	19.8	0.4	88	6	AR146938	AR146938 Sequence
999	19.8	0.4	88	6	AX022112	AX022112 Sequence
1000	19.8	0.4	88	6	AX039313	AX039313 Sequence

ALIGNMENTS

RESULT 1
LOCUS D1D1DKD
DEFINITION D discoideum protein kinase 4 gene, partial cds.
ACCESSION M59747.1 GI:167723
VERSION M59747.1
KEYWORDS protein kinase 4.
SOURCE Dictyostelium discoideum (strain AX-3) DNA.
ORGANISM Dictyostelium discoideum

REFERENCE
AUTHORS Haribabu, B. and Doltin, R. P.
TITLE Identification of a protein kinase multigene family of Dictyostelium discoideum: molecular cloning and expression of a cDNA encoding a developmentally regulated protein kinase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1115-1119 (1991)
MEDLINE 91142122
PUBMED 1996312
FEATURES
source location/Qualifiers
1..87
/organism="Dictyostelium discoideum"
/strain="AX-3"
/db_xref="taxon:44689"
CDS
1..>87
/codon_start=1
/product="protein kinase 4"
/protein_id="AAA3189.1"
/db_xref="GI:167724"
/translation="NLIDYGHILDFGPAKRTENTSMC"

BASE COUNT
ORIGIN
36 a 12 c 14 g 25 t

Query Match
Best Local Similarity 59.5%; Pred. No. 2.5e+04;
Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 4051 AATATCTTCCTTACCTGATTCGATTATCAACGAGGAGTTTGGATGTCAGTAAAG 4110
Db 1 AATCTATTTATGATGATCATATGATGATTTAAGCTACAGATTTTGGATTTGCAAAAAGA 60
QY 4111 CTCAAAACATGATCCACACCATG 4134
Db 61 ATCACAGAGAAATACCAAAAGTATG 84

RESULT 2
LOCUS AR007403 100 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 4 from patent US 5750497.
ACCESSION AR007403
VERSION AR007403.1 GI:3966887
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 100)
AUTHORS Havelund, S., Halstr. o slashed. m, J., Jonassen, I., Andersen, A. Sloth. and Mairussen, J.
TITLE Acylated Insulin
JOURNAL Patent: US 5750497-A 4 12-MAY-1998;
FEATURES Location/Qualifiers
source 1..100
/organism="unknown"
BASE COUNT 29 a 22 c 23 g 26 t
ORIGIN

Query Match
Best Local Similarity 55.6%; Pred. No. 2.3e+05;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 4469 AAGATGAGAGCCTACTAGATATGACTTGGAATATCTTAACTACTGATGATGA 4528
Db 97 AAGTCTGACGAGGCTAAGGATATGCTTGACACATCTGTACTTCTATCTCTTTGTAC 38
QY 4529 TATTACATTAAGACTGCTGAGAGCAG 4558
Db 37 CAATGGAAGAACTACTGTCTTACACGAG 8

RESULT 3
LOCUS AX381834 81 bp DNA linear PAT 18-MAR-2002

DEFINITION Sequence 772 from Patent WO0212280.
 AX381834
 VERSION AX381834.1 GI:19576656
 KEYWORDS
 SOURCE Homo sapiens
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 Pyle, R.A., Xu, J. and Secrist, H.
 AUTHORS Compositions and methods for the therapy and diagnosis of colon
 TITLE Cancer
 JOURNAL Patent: WO 0212280-A-772 14-FEB-2002;
 CORIXA CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..81
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 9 a 22 c 15 g 33 t 2 others
 ORIGIN
 Query Match 0.5%; Score 25.8; DB 6; Length 81;
 Best Local Similarity 57.0%; Pred. No. 2.6e+05;
 Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 Oy 3723 CACCTGCATCAGCGTCGACCGGACCTGATGCGCATGAAAGATTGCAATTCACACC 3782
 Db 79 CACGACAGACGAGGTACCTTTGGGAGCAGAGGCCAATMAAAGTTCAAGTCAAAA 20
 Oy 3783 TAATGACCATTAAGACTATG 3801
 Db 19 AAAAAAAAAAGGCGCNC 1
 RESULT 4
 AF025984 96 bp DNA linear VPR 30-OCT-1997
 LOCUS Paracanthus dentatus lactate dehydrogenase (LDHA) gene, allele
 DEFINITION POLDHA2, Intron 6.
 ACCESSION AF025984
 VERSION AF025984.1 GI:2570847
 KEYWORDS
 SOURCE Paracanthus dentatus.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorphi; Acanthopterygii; Percomorphi; Pleuronectiformes;
 Pleuronectoidae; Paracanthidae; Paracanthus.
 REFERENCE 1 (bases 1 to 96)
 AUTHORS Quattro, J.M. and Jones, W.J.
 TITLE Amplification Primers That Target Locus-Specific Introns in
 TITLE Actinopterygian Fishes
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 96)
 AUTHORS Quattro, J.M. and Jones, W.J.
 TITLE Direct Submission
 JOURNAL Submitted (32-SEP-1997) Biological Sciences, University of South
 Carolina, Coker Life Sciences Building, Columbia, SC 29208, USA
 FEATURES Location/Qualifiers
 source 1..96
 /organism="Paracanthus dentatus"
 /db_xref="taxon:66718"
 gene 1..96
 /gene="LDHA"
 /note="Lactate dehydrogenase gene"
 /allele="POLDHA2"
 1..96
 /gene="LDHA"
 /number=6
 BASE COUNT 24 a 22 c 20 g 30 t
 ORIGIN
 Query Match 0.5%; Score 25.4; DB 5; Length 96;

Best Local Similarity 64.4%; Pred. No. 3.4e+05;
 Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
 Oy 4423 GCCAGCGAGCTCTCGACCATTCGTTGTGTCACAGATGAGAGAGACCT 4481
 Db 14 CTCGACAAATCTAGACGATTCATTACAAACAGTGTGACATGATGATGATGCT 72
 RESULT 5
 AX486379 65 bp DNA linear PAT 16-AUG-2002
 LOCUS Sequence 3679 from Patent WO02053728.
 DEFINITION
 ACCESSION AX486379
 VERSION AX486379.1 GI:22320595
 KEYWORDS
 SOURCE Candida albicans.
 ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitospore Saccharomycetales; Candida.
 REFERENCE 1 Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.
 AUTHORS Gene disruption methodologies for drug target discovery
 TITLE Patent: WO 02053728-A 3679 11-JUL-2002;
 JOURNAL Elitza Pharmaceuticals, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..65
 /organism="Candida albicans"
 /db_xref="taxon:5476"
 BASE COUNT 14 a 5 c 22 g 24 t
 ORIGIN
 Query Match 0.5%; Score 25.2; DB 6; Length 65;
 Best Local Similarity 62.9%; Pred. No. 3.8e+05;
 Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 Oy 712 TATGGAGCTTCGCTGCTTATGAGATGAGAGCTTTATGATGATTCAGTACAGAGG 771
 Db 1 TTGGGACTTTCACCTTTTAAGTCTGAGAGTGGCAGTATGATGATGATGATGAGTGG 60
 Oy 772 CA 773
 Db 61 GA 62
 RESULT 6
 AX033167 70 bp DNA linear BCT 21-SEP-2000
 LOCUS Sequence 3 from Patent WO0045176.
 DEFINITION
 ACCESSION AX033167
 VERSION AX033167.1 GI:10280029
 KEYWORDS
 SOURCE Escherichia coli.
 ORGANISM Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia coli.
 REFERENCE 1 (bases 1 to 70)
 AUTHORS Gallusser, A., Karl, J., Lill, H., Stahl, P., Krueger, R. and Borgya, A.
 TITLE Method of identifying n-terminal probp
 JOURNAL Patent: WO 0045176-A 03-AUG-2000;
 GALUSSER, ANDREAS (DE); KARL, JOHANN (DE); LILL, HELMUT (DE);
 STAHL, PETER (DE); KRUEGER, KERSTIN (DE); BORGYA, ANNETLESE (DE);
 ROCHER, DIAGNOSTICS (DE)
 FEATURES Location/Qualifiers
 source 1..70
 /organism="Escherichia coli"
 /db_xref="taxon:562"
 BASE COUNT 10 a 19 c 21 g 20 t
 ORIGIN
 Query Match 0.5%; Score 25.2; DB 1; Length 70;
 Best Local Similarity 62.9%; Pred. No. 3.8e+05;
 Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

OY	1778	AGGCGGGCCCTGCATGACCACTACTACCAGTTCAATGTGACGAGAGTTCGGAGGACT	1837
Dδ	8	AGGAGAGTCTGTTCACCTCAGTGAGACAGTTTACCCCTGAGGAGGTTACGCTGTTC	67
OY	1838	TG 1839	
Dδ	68	TG 69	

RESULT	7		
LOCUS	AX033159	70 bp	DNA
DEFINITION	Sequence 3 from Patent W00045176.		
ACCESSION	AX033159		linear
VERSION	AX033159.1		PAT 21-SEP-2000
SOURCE	GI:10280023		
ORGANISM	Escherichia coli.		
	Escherichia coli		

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 70)	Gallusser, A., Karl, J., Lill, H., Stahl, P., Krueger, K. and Borgya, A.	Method of identifying n-terminal probsp	Patent: WO 0045176-A 3 03-AUG-2000;

FEATURES	
source	ROCHE DIAGNOSTICS GMBH (DE)
	Location/Qualifiers
	1..70

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/organism="Escherichia coli"
/db_xref="taxon:562"
BASE COUNT      10 a      19 c      21 g      20 t
ORIGIN

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Query Match	0.5%	Score 25.2	DB 6	Length 70
Best Local Similarity	62.9%	Pred. No. 3.8e+05		
Matches	39	Conservative	0	Mismatches 23
				Indels

[illegible]

68 TG 69

LOCUS	SEQUENCE	bp	DNA	linear	PAT
LOCUS	165769	5	99		07-OCT-1997
DEFINITION	Sequence	5	bp		
CESSION	165769		5668294.		
VERSION	165769.1		GI:2482339		
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	unknown.				

REFERENCE
1 (bases 1 to 99)
unclassified.
Meagher, R. B. and Summers, A. O.
TITLE
Metal resistance sequences and transgenic plants
JOURNAL
Patent: US 5668294-A 5 16-SEP-1997;
FEATURES
Location/Qualifiers
SOURCE
1

BASE COUNT	/organism="unknown"
29 a	21 c
	25 g
	24 t

Query Match	0.58;	Score 25.2;	DB 6;	Length 99;
Best Local Similarity	54.38;	Pred. No. 3.9e+05;		
Matches	51; Conservative	0; Mismatches	43;	Indels

AIGUCCTGACTAAATGTAGAGTGGTGACAGGTACACAACCAGGTGGCGACTCAAGCAT

3026
| | | | |
| | | | | | | | | | | | | | | | | |
3085

Db 2 AAGACCCAGCTAAVAGGTGAAGCTGTACTGCTGCATTGGCATGGAAGCATTTCAAGTGC 61
QY 3086 TTGATTTTCTACAGCAATTCGACTGCTTTAT 3119
||| | ||||| | ||||| ||
Db 62 GTGAGCATCTACTCAAGCAAGCCAAAGTGCGCATATAT 95

RESULT 9			
LOCUS			
RABPFKM18			
DEFINITION	83 bp	DNA	linear
ACCESSION	RABPFKM18		MM 27-Apr-1993
VERSION	M14473.1		
KEYWORDS	phosphofructokinase, exon 18.		
SEGMENT	18 of 22		
SOURCE	Rabbit (New Zealand)		
ORGANISM	Oryctolagus cuniculus	DNA, clone lambda-Charon 4APK.	

REFERENCE
1. (pages 1 to 83)
Lee, C.P., Kao, M.C., French, B.A., Putney, S.D. and Chang, S.H.
The rabbit muscle phosphofructokinase gene. Implications for
protein structure, function, and tissue specificity
J. Biol. Chem. 262 (9), 4195-4199 (1987)
87166033

Draft entry and computer-readable sequence for [1] kindly provided by S.H.Chang, 02-FEB-1987.
10004156-00011671.

Source

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/organism="Oryctolagus cuniculus
/db_xref="taxon:9986"
<1. .15
intron

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/note="PFK intron Q"
16. .77
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78. .>83
/seqs="env"

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BASE COUNT	23 a	13 c	27 g	/note="Prk Intron R
RGIN	About 719 bp after segment 17			

Query Match	0.58;	Score 25;	DB 4;	Length 83;
Best Local Similarity	61.5%;	Pred. No. 4.3e+05;		
Matches 40;	Conservative	0;	Mismatches 25;	Indels 0;
				Gaps 0

1737 GAGTATT AAGCAGCTGGTGAGAGAGTGAAGAGAGGCTCTGAAGGGCGCCCTGCTGATGAA 1791
18 GATGTTGAACACCTGGTGCCAAAGATGAAGAGAGACTGTGAAGAGAGAGCTTGGTGCTCGAG 77

1797	GCAGT	180
78	GTACT	82

[illegible]

synthetic construct,
synthetic construct
artificial sequences.
1 (bases 1 to 92)

TITLE Use of recombinant parainfluenza viruses (pIvs) as vaccines in the control of influenza in man and animals

protect against infection and disease caused by HIV and other human pathogens
Patent: WO 0142445-A 31 14-JUN-2001;
The Secretary of the Department of Health and Human Services (US)
Location/Qualifiers

QY	4898 T	4898
	1	
Db	61 T	61

RESULT 19			
092173/c			
LOCUS	51 bp	mRNA	linear
DEFINITION	092173		ROD 19-EBB-1998
	Mus musculus clone IC3 T cell receptor beta chain mRNA, partial		
	cas		

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 31)	Johnston, S. L. and Wettstein, P. J.	T cell receptor diversity in CTLs specific for the CTT-1 and CTT-2 minor histocompatibility antigens	J. Immunol. 159 (6), 2606-2615 (1997)

JOURNAL Submitted (08 MAR 2007) 21:00:00
ROCHESTER MN 55905, USA
LOCATION/QUALIFIERS 1
FEATURES 53

RESULT 20				
LOCUS	AX483371			
DEFINITION	Sequence 671 from Patent WO02053728.	65 bp	DNA	linear
ACCESSION	AX483371			
VERSION	AX483371.1	GI:22317791		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	1 Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlson, K. L.			
TITLE	Gene disruption methodologies for drug target discovery			
JOURNAL	Patent: WO 02053728-A 671 11-JUL-2002;			
	Elitra Pharmaceuticals, Inc. (US)			
FEATURES				
SOURCE	1..65			
	location/Qualifiers			

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/organism="Candida albicans"
/db_xref="taxon:5476"
23 a      2 c      20 g      20 t
BASE COUNT
ORIGIN

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RESULT 21	AX207310	LOCUS	AX207310	66 bp	DNA	linear	* PAT 30-AUG-2001
DEFINITION	Sequence	35	from Patent W00155371.				

	source	1..100	/organism="synthetic construct"	
			/db_xref="taxon:32630"	
BASE COUNT			/note="transcriptional regulatory element"	
ORIGIN	13 a	14 c	22 g	17 t

QY	4855	TTGA	4858
Db	61	TGGA	64

RESULT 22				PRI 04-AUG-2001
AB04840S11				
LOCUS	AB04840S11			
DEFINITION	Homo sapiens PPDEIIA gene, exon 11.			
ACCESSION	AB048411			
VERSION	AB048411.1	GI:15128469		
KEYWORDS				
SEGMENT				
SOURCE	11 of 23 Homo sapiens DNA.			
ORGANISM	Homo sapiens			
TITLE	PPDEIIA; Mus musculus			
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hemo.			
AUTHORS	Yusua,K., Kanoh,Y., Okumuta,K. and Omori,K.			
JOURNAL	Genomic organization of the human phosphodiesterase PPDEIIA gene.			
REFERENCE	Evoluntionary relationship with other PDBs containing GAP domains			
AUTHORS	Eur. J. Biochem. 268 (1), 168-178 (2001)			
TITLE	20570133			
	2 (bases 1 tp 88)			
	Yuasa,K. and Omori,K.			
	Direct Submission			

JOURNAL

Submitted (06-SEP-2000) Kenji Omori, Tanabe Seiyaku Co Ltd.,
Discovery Research Laboratory: 2-50, Kawajishi-2-chome, Toda,
Saitama 335-8505, Japan (E-mail: k-omori@tanabe.co.jp,
Tel:81-48-433-8069, Fax:81-48-433-8159)

FEATURES

Location/Qualifiers

1..88

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="2"

/map="2q31"

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/gene="PDE11A"

/number=10

11..78

/gene="PDE11A"

/note="CDS is reported in Acc# AB048423"

/number=11

79..>88

/gene="PDE11A"

/number=11

28 a 14 c 22 g 24 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 0.5%; Score 24; DB 9; Length 88;

Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1760 AGTGAAGAGGCTCTGAGGCGCGCTGCTGATGAAGACGATCTACCTGATGCTGC 1819

DB 21 AGTGTAAACAGACTGTGGGAAACCTTTGATGATGACATCAACGACTTTTGGAGGT 80

QY 1820 AGGA 1823

DB 81 AAGA 84

RESULT 23

AR014621

LOCUS

DEFINITION Sequence 63 from patent US 5773691.

ACCESSION AR014621

VERSION AR014621.1 GI:3972075

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 97)

AUTORS Falco,S.C., Keeler,S.J., and Rice,J.A.

TITLE Chimeric genes and methods for increasing the lysine and threonine

JOURNAL Patent: US 5773691-A 63 30-JUN-1998;

FEATURES Location/Qualifiers

1..97

BASE COUNT 36 a 5 c 43 g 13 t

ORIGIN

Query Match

Best Local Similarity 0.5%; Score 24; DB 6; Length 97;

Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1120 GAGTATGAGGCTGATGACACAGAGGATTAAGAGAGTTGAAAGTAGTAGGATGAG 1179

DB 10 GAGATGAGAGGCGATGAGAGAGATGAAGATGAAGATGAAGATGAAGATGAAGATGA 69

QY 1180 AGTGAAGAGAA 1191

DB 70 AGAGAGAGATGAA 81

RESULT 24

BD010413

LOCUS

DEFINITION Sequence 63 from patent US 5773691.

ACCESSION BD010413

VERSION BD010413.1 GI:18638786

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTORS

TITLE

JOURNAL

FEATURES

source

1..97

BASE COUNT 36 a 5 c 43 g 13 t

ORIGIN

Query Match

Best Local Similarity 0.5%; Score 24; DB 6; Length 97;

Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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QY 1180 AGTGAAGAGAA 1191

DB 70 AGAGAGAGATGAA 81

RESULT 25

126754

LOCUS

DEFINITION Sequence 54 from patent US 555923.

ACCESSION 126754

VERSION 126754.1 GI:1606624

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTORS

TITLE

JOURNAL

FEATURES

source

1..97

BASE COUNT 36 a 5 c 43 g 13 t

ORIGIN

Query Match

Best Local Similarity 0.5%; Score 24; DB 6; Length 97;

Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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QY 1180 AGTGAAGAGAA 1191

DB 70 AGAGAGAGATGAA 81

RESULT 24

BD010413

LOCUS

DEFINITION Sequence 63 from patent US 5773691.

ACCESSION BD010413

VERSION BD010413.1 GI:18638786

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTORS

TITLE

JOURNAL

FEATURES

source

1..97

BASE COUNT 36 a 5 c 43 g 13 t

ORIGIN

Query Match

DEFINITION

Chimeric genes and methods for increasing the lysine content of the
seeds of plants Chimeric genes and methods for increasing the
lysine content of the seeds of plants Chimeric genes and methods
for increasing the lysine content of the seeds of plants Chimeric
genes and methods for increasing the lysine content of the seeds
of plants.

ACCESSION

BD010413

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTORS

TITLE

JOURNAL

COMMENT

OS

PN

PD

PR

PI

PC

CC

FT

CDS

Location/Qualifiers

1..97

BASE COUNT 36 a 5 c 43 g 13 t

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Query Match

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QY 1120 GAGTATGAGGCTGATGACACAGAGGATTAAGAGAGTTGAAAGTAGTAGGATGAG 1179

DB 10 GAGATGAGAGGCGATGAGAGAGATGAAGATGAAGATGAAGATGAAGATGAAGATGA 69

QY 1180 AGTGAAGAGAA 1191

DB 70 AGAGAGAGATGAA 81

RESULT 25

126754

LOCUS

DEFINITION Sequence 54 from patent US 555923.

ACCESSION 126754

VERSION 126754.1 GI:1606624

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTORS

TITLE

JOURNAL

FEATURES

source

1..97

BASE COUNT 36 a 5 c 43 g 13 t

ORIGIN

Query Match

Best Local Similarity 0.5%; Score 24; DB 6; Length 97;

Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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DB 10 GAGATGAGAGGCGATGAGAGAGATGAAGATGAAGATGAAGATGAAGATGAAGATGA 69

QY 1180 AGTGAAGAGAA 1191

DB 70 AGAGAGAGATGAA 81

RESULT 25

126754

LOCUS

DEFINITION Sequence 54 from patent US 555923.

ACCESSION 126754

VERSION 126754.1 GI:1606624

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTORS

TITLE

JOURNAL

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source

1..97

BASE COUNT 36 a 5 c 43 g 13 t

ORIGIN

Query Match

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DB 70 AGAGAGAGATGAA 81

RESULT 25

126754

LOCUS

DEFINITION Sequence 54 from patent US 555923.

ACCESSION 126754

VERSION 126754.1 GI:1606624

KEYWORDS

SOURCE

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REFERENCE

AUTORS

TITLE

JOURNAL

FEATURES

source

1..97

BASE COUNT 36 a 5 c 43 g 13 t

ORIGIN

Query Match

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Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1120 GAGTATGAGGCTGATGACACAGAGGATTAAGAGAGTTGAAAGTAGTAGGATGAG 1179

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QY 1180 AGTGAAGAGAA 1191

DB 70 AGAGAGAGATGAA 81

RESULT 25

126754

LOCUS

DEFINITION Sequence 54 from patent US 555923.

ACCESSION 126754

VERSION 126754.1 GI:1606624

KEYWORDS

SOURCE

ORGANISM

REFERENCE

Wed Nov 13 14:22:40 2002

us-09-676-436-3.liml.rge

Page 15

Best Local Similarity 58.3%; Pred. No. 8.2e+05; Mismatches 30; Indels 0; Gaps 0;
Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
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DB 10 GAAGATGAGAGGCGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 69
OY 1180 AGTGAAGAAGAA 1191
DB 70 AGAGAAGATGAA 81
RESULT 26 AF294354S 82 bp DNA linear MAM 03-OCT-2000
LOCUS AF294354S
DEFINITION Bos taurus hypoxanthine phosphoribosyltransferase (HPRT) gene, exon 5.
ACCESSION AF294358.1 GI:10505250
VERSION AF294358.1
KEYWORDS 5 of 7
SEGMENT Bos taurus.
SOURCE Bos taurus.
ORGANISM Bos taurus.
REFERENCE 1 (bases 1 to 82) Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
AUTHORS Poloumienko, A. and Blecher, S.R.
TITLE Exon-intron structure of mammalian HPRT genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 82) Poloumienko, A.
AUTHORS Direct Submission
TITLE Submitted (09-AUG-2000) Molecular Biology and Genetics, University of Guelph, Axelrod Building, Guelph, Ontario N1G 2W1, Canada
FEATURES
SOURCE Location/Qualifiers
1..82
/organism="Bos taurus"
/db_xref="taxon:9913"
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/sex="female"
/tissue_type="liver"
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/gene="HPRT"
exon
number=5
28 a 14 c 21 g 19 t
BASE COUNT
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Best Local Similarity 62.7%; Pred. No. 9.2e+05; Mismatches 22; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
OY 178 GACACTGGAACACAGTGAAGATGTGAGAGATATACAGCTATAGCAGAGAGAGAGAT 236
DB 9 GACACTGGAACACAGTGAAGATGTGAGAGATATACAGCTATAGCAGAGAGAGAGAT 67
RESULT 27 AF050514 87 bp DNA linear VRL 12-MAR-1998
LOCUS AF050514
DEFINITION Human endogenous retrovirus clone 19P reverse transcriptase gene, partial cds.
ACCESSION AF050514.1 GI:2952454
VERSION AF050514.1
KEYWORDS Human endogenous retrovirus.
SOURCE Human endogenous retrovirus.
ORGANISM Human endogenous retrovirus.
REFERENCE 1 (bases 81 to 87) Rose, J., and Henikoff, S.
AUTHORS McCullum, C.M. and Henikoff, S.
TITLE Consensus-degenerate hybrid oligonucleotide primers for amplification of distantly-related sequences

JOURNAL Nucleic Acids Res. (1998) In press
REFERENCE 2 (bases 1 to 87)
AUTHORS Rose, J., Schultz, E.R., Henikoff, J.G., Pietrokovski, S., McCullum, C.M., and Henikoff, S.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-1998) Fred Hutchinson Cancer Research Center, 1100 Fairview Ave., N. Seattle, WA 98109-1024, USA
FEATURES
SOURCE location/Qualifiers
1..87
/organism="Human endogenous retrovirus"
/db_xref="taxon:11827"
/clone="19P"
/note="isolated from a Kaposi's sarcoma lesion"
CDS
1..87
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Matches 43; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
OY 3768 GATTCGATTTCAACCTATGACCATATGACATATGACATATGACATATGACATATGACAT 3827
DB 12 GACTATTTGCAAACTTATGTCGAAAGCTATTAAGCAGTTAGAGACATTTAATAA 71
OY 3828 ATTGGAAGCATCAA 3842
DB 72 ATGTTATATCATCA 86
RESULT 28 TRBANTATC2 90 bp mRNA linear INV 26-APR-1993
LOCUS TRBANTATC2
DEFINITION Trypanosoma brucei Antat 1.3A C2 mRNA, 5' end.
ACCESSION M28495
VERSION M28495.1 GI:161984
KEYWORDS Trypanosoma brucei
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
REFERENCE 1 (bases 1 to 90) Cognielet, H., Tebbi, P., Pays, A., Steiner, M., and Pays, E.
AUTHORS Trypanosoma brucei: enrichment by UV of intergenic transcripts from the variable surface glycoprotein gene expression site
JOURNAL Mol. Cell. Biol. 9 (9), 4022-4025 (1989)
MEDLINE 89384631
PubMed 2779575
FEATURES
SOURCE location/Qualifiers
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/db_xref="taxon:5691"
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Matches 46; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
OY 1360 TGTCTGACTTCTATTATAGACATTTGATGACAAAGCAGCAGAGAGGGGTTAAG 1419
DB 6 TATCTTACCATGACAGCAAAATTTTCTGCTGATGATGATGATGATGATGATGATGAT 65

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
1,9 OF 31	Homo sapiens.			
	Homo sapiens			
	Eukaryota; Metazoa;			
	Chordata; Craniota;			
	Vertebrata; Euteleostomi;			
	Mammalia; Eutheria;			
	Primates; Catarrhini;			
	Hominae; Homo.			
	(bases 1 to 94)			
	Fleming, J.C., Pahl, H.L.,			
	Gonzalez, D.A., Smith, T.F.			
	and Tenen, D.G.			
	Structural analysis of the CD1b gene and phylogenetic analysis of			

detection of binding reactions

JOURNAL Patient: US 5843767-A 4 01-DEC-1998;
 FEATURES Location/Qualifiers
 source 1..87
 BASE COUNT 24 a 10 c 18 g 32 t 3 others
 ORIGIN 10 c 18 g 32 t 3 others

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 Best Local Similarity 57.6%; Pred. No. 1e+06;
 Matches 38; Conservative 2; Mismatches 26; Indels 0; Gaps 0;

QY 3801 CAAGAACTGCAGCAAGATTGAATATATCGAAGCATCAACACCCCAATCTGCTCG 3860
 Db 83 CATTCATATYCTGAGTATATCATTTATAGCAAGCATATCCWACACAACTTGTCTG 24
 QY 3861 GTATTT 3866
 Db 23 GAATTT 18

RESULT 36
 HUMUT770A 88 bp DNA linear STS 29-DEC-1994
 LOCUS Human STS UT770, 5' primer bind, sequence tagged site.
 DEFINITION L31186
 ACCESSION L31186
 VERSION L31186.1 GI:605227
 KEYWORDS STS; PCR primer; STS sequence: microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 88)
 AUTHORS Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen,H., Ballard,L., Melis,R., Lawrence,E., Moore,M., Holik,P.R., Carlson,M., Zhao,X., Robertson,M., Bradley,P., Elsnier,T., Tingey,A., Lalouel,J.-M. and White,R.
 TITLE Genetic and physical mapping of simple sequence repeat containing unpublished (1994)
 COMMENT Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
 2160 Eccles Institute of Human Genetics
 Salt Lake City, UT 84112
 e-mail: steecorona.med.utah.edu
 Primer A: GCGTGGTAATAGAGCAG
 Primer B: CACATTTCCTTACAC
 End to label: Primer B
 PCR Profile:
 Initial Denaturation: 94C 300sec
 Cycles Denaturation Annealing Extension
 C 10 sec. 58 C 10 sec. 72 C 20 sec. 31 94
 54 C 10 sec. 72 C 20 sec. Mg++: 3.00 mM
 Gel: Acrylamide 7%, Formamide 32%, Urea 34%
 Alleles: 4.

FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 primer_bind 18..36
 /db_xref="taxon:9606"
 BASE COUNT 35 a 13 c 20 g 10 t 10 others
 ORIGIN 13 c 20 g 10 t 10 others

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 Best Local Similarity 52.6%; Pred. No. 1e+06;
 Matches 41; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 476 TTGAACCTTACACATTTTGTAAAGCTTACCTACAGTCTCAAGAAAGAGAGGAGC 535
 Db 7 TTGCACCTCTACGCTGGTAATAGAGCAGANTCAGTCAAAAAGAGAGAGAGAGAGA 66
 QY 536 AAGAGGACAGAAATA 553

Db 67 NAGANAGANAGANAGANA 84

RESULT 37
 AX326603/c 98 bp DNA linear PAT 07-JAN-2002
 LOCUS AX326603
 DEFINITION Sequence 24 from Patent WO0192579.
 ACCESSION AX326603
 VERSION AX326603.1 GI:18097366
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
 AUTHORS Wenz,H.M. and Schroth,G.P.
 TITLE Methods for detecting target nucleic acids using coupled ligation and amplification
 JOURNAL Patent: WO 0192579-A 24 06-DEC-2001;
 PE Corporation (NY) (US)

FEATURES Location/Qualifiers
 source 1..98
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /note="Chromosome Chr.6, 217.4 CR; GenBank number AW675467; Unigene description/ID: splicing factor, arginine/serine-rich 3 (SFRS3)/hs.167460-allele of SEQ ID NO: 25"

BASE COUNT 23 a 14 c 20 g 41 t

Query Match 0.5%; Score 23.6; DB 6; Length 98;
 Best Local Similarity 53.2%; Pred. No. 1e+06;
 Matches 50; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 4527 AATATTACATAAAGCTGTCGACAGACGATATAGCTTTTAACCTTCCAGACTG 4586
 Db 94 AATTGACATTAAGATGTGACAGACCATGTATCATATACAGCAATCAATAAAG 35
 QY 4587 AAGACGTGACAGGTGACAAAGCTCACTTCTCTG 4620
 Db 34 AACTTATGACCTTAAGCAAGCTTAACCTTCTG 1

RESULT 38
 AX059602 99 bp DNA linear PAT 22-JAN-2001
 LOCUS AX059602
 DEFINITION Sequence 10 from Patent WO0078963.
 ACCESSION AX059602
 VERSION AX059602.1 GI:12405450
 KEYWORDS unidentified.
 SOURCE unidentified.
 ORGANISM unidentified.

REFERENCE 1 (bases 1 to 99)
 AUTHORS Mijert,H.J., Stinder,L. and Kreutzmann,P.
 TITLE Serin proteinase inhibitors
 JOURNAL Patent: WO 0078963-A 10 28-DEC-2000;
 FORSSMANN, Wolf-Georg (DE)

FEATURES Location/Qualifiers
 source 1..99
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 /note="Mammalia"
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 ORIGIN 20 c 22 g 21 t

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 Best Local Similarity 58.6%; Pred. No. 1e+06;
 Matches 41; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 3657 GAGGAGGTGACCTTCAATGTGCAAGAGCAACAAATTTGGAGAGGCCGATATGGAA 3716

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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 07:04:10 : Search time 109 seconds
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14039.606 Million cell updates/sec

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Perfect score: 4990
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Scoring table: IDENTITY_NUC
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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 684418

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Maximum DB seq length: 100

Post-processing: Minimum Match 0%
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	26	0.5	100	1	US-08-400-256-4
C 3	25.2	0.5	99	1	US-08-427-097-5
C 4	25.2	0.5	99	1	US-08-427-097-5
C 5	24.8	0.5	47	4	US-09-641-638-918
C 6	24.6	0.5	71	1	US-08-458-423A-78
C 7	24.6	0.5	71	1	US-08-458-423A-78
C 8	24.6	0.5	71	1	US-08-458-423A-78
C 9	24.6	0.5	71	1	US-08-458-423A-78
C 10	24.6	0.5	72	3	US-09-100-664A-5
C 11	24.6	0.5	72	3	US-09-100-664A-5
C 12	24.6	0.5	98	4	US-09-506-729-21
C 13	24.4	0.5	100	3	US-08-400-256-9
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C 17	24.4	0.5	97	1	US-08-975-365-9
C 18	24.4	0.5	97	1	US-08-975-365-9
C 19	23.8	0.5	83	1	US-08-823-771-63
C 20	23.8	0.5	83	1	US-08-823-771-63
C 21	23.4	0.5	83	1	US-08-823-771-63
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C 24	23.2	0.5	47	4	US-09-641-638-918
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C 26	22.8	0.5	60	3	US-08-643-704A-17
C 27	22.6	0.5	76	4	US-08-484-323-5
C 28	22.6	0.5	76	4	US-08-484-323-5
C 29	22.4	0.4	90	1	US-08-123-702-21
C 30	22.4	0.4	95	2	US-08-332-766A-41
C 31	22.4	0.4	97	1	US-08-182-175A-48
C 32	22.4	0.4	97	1	US-08-474-633A-57
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C 34	22.2	0.4	97	5	US-09-202-06412-48
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C 73	21.2	0.4	71	2	US-08-465-591A-75
C 74	21.2	0.4	71	2	US-08-465-591A-75
C 75	21.2	0.4	71	2	US-08-465-591A-75
C 76	21.2	0.4	71	2	US-08-465-591A-75
C 77	21.2	0.4	71	2	US-08-465-591A-75
C 78	21.2	0.4	71	2	US-08-465-591A-75
C 79	21.2	0.4	71	2	US-08-465-591A-75
C 80	21.2	0.4	71	2	US-08-465-591A-75
C 81	21.2	0.4	71	2	US-08-465-591A-75
C 82	21.2	0.4	71	2	US-08-465-591A-75
C 83	21.2	0.4	71	2	US-08-465-591A-75
C 84	21.2	0.4	71	2	US-08-465-591A-75
C 85	21.2	0.4	71	2	US-08-465-591A-75
C 86	21.2	0.4	71	2	US-08-465-591A-75
C 87	21.2	0.4	71	2	US-08-465-591A-75
C 88	21.2	0.4	71	2	US-08-465-591A-75
C 89	21.2	0.4	71	2	US-08-465-591A-75
C 90	21.2	0.4	71	2	US-08-465-591A-75
C 91	21.2	0.4	71	2	US-08-465-591A-75
C 92	21.2	0.4	71	2	US-08-465-591A-75
C 93	21.2	0.4	71	2	US-08-465-591A-75
C 94	21.2	0.4	71	2	US-08-465-591A-75
C 95	21.2	0.4	71	2	US-08-465-591A-75
C 96	21.2	0.4	71	2	US-08-465-591A-75
C 97	21.2	0.4	71	2	US-08-465-591A-75
C 98	21.2	0.4	71	2	US-08-465-591A-75
C 99	21.2	0.4	71	2	US-08-465-591A-75
C 100	21.2	0.4	71	2	US-08-465-591A-75

C 101	21	0.4	81	4	US-08-556-978B-91	Sequence 91, Appl	C 174	20.6	0.4	73	1	US-08-257-073-80	Sequence 80, Appl
102	21	0.4	82	1	US-08-832-883-61	Sequence 61, Appl	175	20.6	0.4	73	1	US-08-110-294A-26	Sequence 26, Appl
103	21	0.4	82	2	US-08-832-877-61	Sequence 61, Appl	176	20.6	0.4	73	2	US-08-184-009-13	Sequence 13, Appl
104	21	0.4	84	1	US-07-696-551B-3	Sequence 3, Appl	177	20.6	0.4	73	2	US-08-486-969-13	Sequence 13, Appl
105	21	0.4	86	1	US-08-447-169A-169	Sequence 169, Appl	178	20.6	0.4	73	2	US-08-417-210A-13	Sequence 13, Appl
106	21	0.4	86	2	US-08-477-527A-94	Sequence 94, Appl	179	20.6	0.4	73	2	US-08-389-926-26	Sequence 26, Appl
107	21	0.4	86	3	US-08-481-710-94	Sequence 94, Appl	180	20.6	0.4	73	2	US-08-458-356-13	Sequence 13, Appl
108	21	0.4	86	3	US-09-009-913-287	Sequence 287, App	181	20.6	0.4	73	2	US-08-471-025-13	Sequence 13, Appl
109	21	0.4	86	5	PCT-US96-09537-94	Sequence 94, Appl	182	20.6	0.4	73	3	US-08-473-446-36	Sequence 36, Appl
110	21	0.4	86	5	PCT-US96-09537-94	Sequence 261, App	183	20.6	0.4	73	3	US-08-460-736-13	Sequence 13, Appl
111	21	0.4	86	5	US-09-404-879A-261	Sequence 1122, App	184	20.6	0.4	73	4	US-08-354-18-13	Sequence 13, Appl
112	20.8	0.4	54	1	US-08-311-486C-1122	Sequence 11, Appl	185	20.6	0.4	73	5	PCT-US96-00547-13	Sequence 13, Appl
113	20.8	0.4	60	4	US-09-388-128-1	Sequence 17, Appl	186	20.6	0.4	77	4	US-09-330-245A-3	Sequence 3, Appl
114	20.8	0.4	60	5	PCT-US95-11985A-17	Sequence 8, Appl	187	20.6	0.4	78	1	US-08-477-877B-62	Sequence 62, Appl
115	20.8	0.4	63	3	US-09-029-267-8	Sequence 8, Appl	188	20.6	0.4	78	1	US-08-472-281A-62	Sequence 62, Appl
116	20.8	0.4	63	5	PCT-US91-03680-8	Sequence 3, Appl	189	20.6	0.4	78	2	US-08-477-989B-62	Sequence 62, Appl
117	20.8	0.4	68	4	US-09-308-246C-3	Sequence 8, Appl	190	20.6	0.4	78	3	US-08-933-983-49	Sequence 49, Appl
118	20.8	0.4	70	4	US-08-584-760A-4	Sequence 4, Appl	191	20.6	0.4	78	3	US-08-933-983-69	Sequence 49, Appl
119	20.8	0.4	70	4	US-08-584-760A-7	Sequence 7, Appl	192	20.6	0.4	80	4	US-09-149-1727-49	Sequence 49, Appl
120	20.8	0.4	79	1	US-08-208-866C-37	Sequence 37, Appl	193	20.6	0.4	81	1	US-08-238-863-34	Sequence 34, Appl
121	20.8	0.4	79	1	US-08-704-774-37	Sequence 37, Appl	194	20.6	0.4	81	1	US-08-472-255A-164	Sequence 164, Appl
122	20.8	0.4	79	2	US-08-469-557-37	Sequence 37, Appl	195	20.6	0.4	81	1	US-08-479-724A-164	Sequence 164, Appl
123	20.8	0.4	80	4	US-08-290-793B-37	Sequence 22, Appl	196	20.6	0.4	81	1	US-08-443-407-34	Sequence 34, Appl
124	20.8	0.4	81	1	US-08-399-412A-85	Sequence 85, Appl	197	20.6	0.4	81	3	US-08-472-266B-164	Sequence 164, Appl
125	20.8	0.4	83	1	US-08-420-443-5	Sequence 5, Appl	198	20.6	0.4	81	4	US-08-952-793-164	Sequence 164, Appl
126	20.8	0.4	83	1	US-08-411-796-93	Sequence 93, Appl	199	20.6	0.4	81	4	US-09-487-253A-28	Sequence 28, Appl
127	20.8	0.4	83	3	US-08-471-039-93	Sequence 93, Appl	200	20.6	0.4	81	5	PCT-US95-05600-178	Sequence 178, Appl
128	20.8	0.4	83	5	PCT-US93-11198-93	Sequence 88, Appl	201	20.6	0.4	81	5	PCT-US96-00455A-114	Sequence 114, Appl
129	20.8	0.4	84	1	US-08-182-175A-88	Sequence 88, Appl	202	20.6	0.4	86	1	US-08-447-169A-210	Sequence 210, Appl
130	20.8	0.4	84	1	US-08-182-175A-89	Sequence 89, Appl	203	20.6	0.4	87	1	US-08-433-126A-215	Sequence 215, Appl
131	20.8	0.4	84	1	US-08-182-175A-88	Sequence 89, Appl	204	20.6	0.4	87	1	US-08-433-126A-215	Sequence 215, Appl
132	20.8	0.4	84	1	US-08-474-633A-65	Sequence 65, Appl	205	20.6	0.4	87	1	US-08-433-126A-215	Sequence 215, Appl
133	20.8	0.4	84	1	US-08-474-633A-65	Sequence 66, Appl	206	20.6	0.4	87	3	US-08-976-113A-215	Sequence 215, Appl
134	20.8	0.4	84	4	US-08-729-601A-34	Sequence 34, Appl	207	20.6	0.4	87	3	FCT-US96-06059-215	Sequence 215, Appl
135	20.8	0.4	84	4	US-08-823-771-65	Sequence 65, Appl	208	20.6	0.4	90	4	US-08-840-666A-24	Sequence 24, Appl
136	20.8	0.4	84	5	US-08-823-771-66	Sequence 66, Appl	209	20.6	0.4	91	2	US-09-696-188B-24	Sequence 24, Appl
137	20.8	0.4	84	5	PCT-US92-06412-88	Sequence 88, Appl	210	20.6	0.4	91	4	US-08-762-106-42	Sequence 42, Appl
138	20.8	0.4	87	4	US-09-364-543-20	Sequence 20, Appl	211	20.6	0.4	94	4	US-09-320-774-42	Sequence 42, Appl
139	20.8	0.4	90	2	US-08-350-260A-594	Sequence 594, App	212	20.6	0.4	96	3	US-08-641-873-18	Sequence 18, Appl
140	20.8	0.4	93	3	US-09-182-859-37	Sequence 37, Appl	213	20.6	0.4	100	1	US-08-145-705A-4	Sequence 4, Appl
141	20.8	0.4	93	3	US-09-672-459-37	Sequence 37, Appl	214	20.6	0.4	100	1	US-08-145-705A-19	Sequence 19, Appl
142	20.8	0.4	95	3	US-08-284-516C-52	Sequence 52, Appl	215	20.4	0.4	69	1	US-07-991-867B-29	Sequence 29, Appl
143	20.8	0.4	95	4	US-09-537-911A-52	Sequence 52, Appl	216	20.4	0.4	69	1	US-08-107-755A-29	Sequence 29, Appl
144	20.8	0.4	97	1	US-08-182-175A-38	Sequence 38, Appl	217	20.4	0.4	69	2	US-08-544-332-29	Sequence 29, Appl
145	20.8	0.4	97	1	US-08-182-175A-42	Sequence 42, Appl	218	20.4	0.4	72	1	US-09-370-861A-39	Sequence 39, Appl
146	20.8	0.4	97	1	US-08-182-175A-46	Sequence 46, Appl	219	20.4	0.4	72	1	US-07-737-071A-3	Sequence 3, Appl
147	20.8	0.4	97	1	US-08-472-255A-22	Sequence 22, Appl	220	20.4	0.4	72	1	US-08-022-096-3	Sequence 3, Appl
148	20.8	0.4	97	1	US-08-474-633A-35	Sequence 35, Appl	221	20.4	0.4	76	1	US-08-384-708A-201	Sequence 201, Appl
149	20.8	0.4	97	1	US-08-474-633A-35	Sequence 35, Appl	222	20.4	0.4	76	1	US-08-447-169A-101	Sequence 101, Appl
150	20.8	0.4	97	1	US-08-474-633A-55	Sequence 55, Appl	223	20.4	0.4	76	2	US-08-233-012C-101	Sequence 101, Appl
151	20.8	0.4	97	1	US-08-479-724A-22	Sequence 22, Appl	224	20.4	0.4	76	2	US-08-687-421-293	Sequence 293, Appl
152	20.8	0.4	97	3	US-08-472-256B-22	Sequence 22, Appl	225	20.4	0.4	81	3	US-09-014-416-57	Sequence 57, Appl
153	20.8	0.4	97	3	US-08-952-793-22	Sequence 22, Appl	226	20.4	0.4	81	3	US-08-332-766A-44	Sequence 44, Appl
154	20.8	0.4	97	4	US-08-823-771-35	Sequence 35, Appl	227	20.4	0.4	89	3	US-09-065-474-132	Sequence 132, Appl
155	20.8	0.4	97	4	US-08-823-771-35	Sequence 35, Appl	228	20.4	0.4	89	3	US-09-065-474-132	Sequence 132, Appl
156	20.8	0.4	97	4	US-08-823-771-35	Sequence 35, Appl	229	20.4	0.4	89	4	US-09-557-034-132	Sequence 132, Appl
157	20.8	0.4	97	5	PCT-US92-06412-38	Sequence 38, Appl	230	20.4	0.4	89	4	US-09-557-034-133	Sequence 133, Appl
158	20.8	0.4	97	5	PCT-US92-06412-42	Sequence 42, Appl	231	20.4	0.4	93	4	US-09-030-607-220	Sequence 220, Appl
159	20.8	0.4	97	5	PCT-US92-06412-46	Sequence 46, Appl	232	20.4	0.4	93	4	US-09-439-313-220	Sequence 220, Appl
160	20.8	0.4	97	5	PCT-US92-06412-46	Sequence 46, Appl	233	20.4	0.4	93	4	US-09-352-616A-220	Sequence 220, Appl
161	20.8	0.4	99	1	US-07-968-971A-9	Sequence 9, Appl	234	20.2	0.4	49	4	US-09-232-149A-220	Sequence 220, Appl
162	20.8	0.4	99	1	US-08-145-705A-33	Sequence 33, Appl	235	20.2	0.4	50	2	US-09-091-814-18	Sequence 18, Appl
163	20.8	0.4	99	4	US-09-421-298-68	Sequence 68, Appl	236	20.2	0.4	50	2	US-08-299-074A-17	Sequence 17, Appl
164	20.8	0.4	100	1	US-08-773-731A-6	Sequence 71, Appl	237	20.2	0.4	57	4	US-09-461-697-428	Sequence 428, Appl
165	20.8	0.4	100	3	US-08-584-040-8223	Sequence 8223, App	238	20.2	0.4	60	4	US-08-470-419-15	Sequence 15, Appl
166	20.6	0.4	54	4	US-09-023-228B-71	Sequence 71, Appl	239	20.2	0.4	60	4	US-08-761-828-15	Sequence 15, Appl
167	20.6	0.4	61	3	US-09-163-025B-71	Sequence 36, Appl	240	20.2	0.4	63	2	US-08-290-105-15	Sequence 15, Appl
168	20.6	0.4	61	3	US-08-220-151-36	Sequence 36, Appl	241	20.2	0.4	63	2	US-08-776-949-15	Sequence 15, Appl
169	20.6	0.4	73	1	US-08-220-151-37	Sequence 36, Appl	242	20.2	0.4	63	3	US-08-482-810-15	Sequence 15, Appl
170	20.6	0.4	73	1	US-08-413-118-36	Sequence 13, Appl	243	20.2	0.4	63	3	US-09-027-955-15	Sequence 15, Appl
171	20.6	0.4	73	1	US-08-224-657-13	Sequence 13, Appl	244	20.2	0.4	63	3		
172	20.6	0.4	73	1			245	20.2	0.4	63	3		
173	20.6	0.4	73	1			246	20.2	0.4	63	4		

247	20.2	0.4	63	4	US-09-636-805-15	Sequence 15, Appl	320	20	0.4	60	2	US-08-288-065A-40	Sequence 40, Appl
248	20.2	0.4	63	4	US-09-258-128-15	Sequence 15, Appl	321	20	0.4	60	2	US-08-362-240A-40	Sequence 40, Appl
249	20.2	0.4	65	3	US-08-445-463B-11	Sequence 11, Appl	322	20	0.4	60	5	PCT-US95-102A-40	Sequence 40, Appl
250	20.2	0.4	65	3	US-08-445-464C-11	Sequence 11, Appl	323	20	0.4	62	4	US-09-116-032-24	Sequence 13, Appl
251	20.2	0.4	65	3	US-08-044-857D-11	Sequence 11, Appl	324	20	0.4	68	1	US-07-795-859B-13	Sequence 13, Appl
252	20.2	0.4	65	5	PCT-US94-03437-11	Sequence 11, Appl	325	20	0.4	70	4	US-08-457-616-13	Sequence 8, Appl
253	20.2	0.4	69	1	US-08-180-195-25	Sequence 25, Appl	326	20	0.4	73	2	US-09-010-928B-8	Sequence 8, Appl
254	20.2	0.4	69	1	US-08-434-001-78	Sequence 25, Appl	327	20	0.4	74	4	US-09-305-408-8	Sequence 8, Appl
255	20.2	0.4	69	1	US-08-477-329-25	Sequence 25, Appl	328	20	0.4	75	5	US-08-195-874-5	Sequence 5, Appl
256	20.2	0.4	69	1	US-08-433-585-78	Sequence 78, Appl	329	20	0.4	75	5	PCT-US95-01671-5	Sequence 5, Appl
257	20.2	0.4	69	2	US-08-475-458-25	Sequence 78, Appl	330	20	0.4	81	2	US-08-451-472-54	Sequence 54, Appl
258	20.2	0.4	69	2	US-08-437-657-78	Sequence 78, Appl	331	20	0.4	81	2	US-08-469-537A-65	Sequence 65, Appl
259	20.2	0.4	69	3	US-08-960-955-78	Sequence 78, Appl	332	20	0.4	82	2	US-08-454-557C-81	Sequence 81, Appl
260	20.2	0.4	69	3	US-08-960-955-78	Sequence 25, Appl	333	20	0.4	82	2	US-08-340-426D-81	Sequence 81, Appl
261	20.2	0.4	69	3	US-08-960-955-78	Sequence 78, Appl	334	20	0.4	82	2	US-08-450-673C-81	Sequence 81, Appl
262	20.2	0.4	69	3	US-08-960-955-78	Sequence 25, Appl	335	20	0.4	82	2	PCT-US95-17111A-81	Sequence 81, Appl
263	20.2	0.4	69	3	US-08-960-955-78	Sequence 25, Appl	336	20	0.4	82	5	US-08-454-557C-91	Sequence 91, Appl
264	20.2	0.4	69	4	US-09-583-410-25	Sequence 25, Appl	337	20	0.4	84	2	US-08-340-426D-91	Sequence 91, Appl
265	20.2	0.4	69	4	US-09-583-410-25	Sequence 25, Appl	338	20	0.4	84	2	US-08-450-673C-91	Sequence 91, Appl
266	20.2	0.4	69	4	US-09-583-410-25	Sequence 25, Appl	339	20	0.4	84	2	US-08-450-673C-91	Sequence 91, Appl
267	20.2	0.4	69	4	US-09-396-002A-78	Sequence 78, Appl	340	20	0.4	88	5	PCT-US95-10973A-36	Sequence 36, Appl
268	20.2	0.4	69	5	PCT-US96-06060-78	Sequence 78, Appl	341	20	0.4	88	5	US-07-964-624D-24	Sequence 24, Appl
269	20.2	0.4	71	1	US-08-180-195-24	Sequence 24, Appl	342	20	0.4	89	1	US-08-476-697A-24	Sequence 24, Appl
270	20.2	0.4	71	1	US-08-477-329-24	Sequence 24, Appl	343	20	0.4	89	1	US-08-165-616-24	Sequence 24, Appl
271	20.2	0.4	71	2	US-08-475-458-24	Sequence 24, Appl	344	20	0.4	89	4	US-09-165-917-41	Sequence 41, Appl
272	20.2	0.4	71	3	US-08-980-400-24	Sequence 24, Appl	345	20	0.4	90	1	US-08-384-616-41	Sequence 41, Appl
273	20.2	0.4	71	4	US-09-583-459A-24	Sequence 24, Appl	346	20	0.4	90	2	US-08-904-686A-41	Sequence 41, Appl
274	20.2	0.4	71	4	US-09-583-459A-24	Sequence 24, Appl	347	20	0.4	90	2	US-09-315-850-41	Sequence 41, Appl
275	20.2	0.4	71	4	US-09-435-059-24	Sequence 24, Appl	348	20	0.4	90	4	US-08-808-331-25	Sequence 25, Appl
276	20.2	0.4	81	1	US-08-183-175A-30	Sequence 30, Appl	349	20	0.4	93	2	US-08-808-331-25	Sequence 25, Appl
277	20.2	0.4	84	1	US-08-823-771-72	Sequence 72, Appl	350	20	0.4	93	3	US-09-050-603A-25	Sequence 25, Appl
278	20.2	0.4	84	1	US-08-823-771-72	Sequence 72, Appl	351	20	0.4	93	3	US-09-102-420B-25	Sequence 25, Appl
279	20.2	0.4	84	5	PCT-US92-06412-30	Sequence 30, Appl	352	20	0.4	93	3	US-09-497-698E-25	Sequence 25, Appl
280	20.2	0.4	87	2	US-08-371-774-101	Sequence 101, Appl	353	20	0.4	94	4	US-08-706-945D-116	Sequence 116, Appl
281	20.2	0.4	87	2	US-08-371-774-101	Sequence 101, Appl	354	20	0.4	95	1	US-08-609-271-9	Sequence 9, Appl
282	20.2	0.4	90	2	US-09-320-774-44	Sequence 44, Appl	355	20	0.4	95	1	US-08-688-649-9	Sequence 9, Appl
283	20.2	0.4	90	4	US-08-461-697-376	Sequence 376, Appl	356	20	0.4	95	1	US-08-438-511-2	Sequence 2, Appl
284	20.2	0.4	90	4	US-08-475-783A-75	Sequence 75, Appl	357	20	0.4	95	2	US-08-188-374-9	Sequence 9, Appl
285	20.2	0.4	95	1	US-08-475-783A-75	Sequence 75, Appl	358	20	0.4	95	2	US-08-188-374-9	Sequence 9, Appl
286	20.2	0.4	95	1	US-08-475-783A-75	Sequence 75, Appl	359	20	0.4	95	2	US-08-973-629-5	Sequence 28, Appl
287	20.2	0.4	95	1	US-08-475-783A-75	Sequence 75, Appl	360	20	0.4	95	3	US-08-954-395A-28	Sequence 47, Appl
288	20.2	0.4	95	3	US-08-869-333F-96	Sequence 96, Appl	361	20	0.4	100	4	US-08-455-968E-47	Sequence 2, Appl
289	20.2	0.4	95	4	US-08-869-333F-96	Sequence 96, Appl	362	20	0.4	41	2	PCT-US91-03540A-2	Sequence 127, Appl
290	20.2	0.4	95	4	US-08-869-333F-96	Sequence 96, Appl	363	20	0.4	60	6	5168050-11	Sequence 4, Appl
291	20.2	0.4	95	4	US-08-869-333F-96	Sequence 96, Appl	364	20	0.4	61	4	US-08-254-968-127	Sequence 20, Appl
292	20.2	0.4	95	5	PCT-US96-08014-164	Sequence 164, Appl	365	20	0.4	63	3	US-08-750-419A-4	Sequence 6, Appl
293	20.2	0.4	96	4	US-09-513-783A-157	Sequence 157, Appl	366	20	0.4	64	5	PCT-US95-05758-20	Sequence 6, Appl
294	20.2	0.4	98	1	US-08-088-658-42	Sequence 42, Appl	367	20	0.4	64	5	US-08-374-641-6	Sequence 6, Appl
295	20.2	0.4	98	1	US-08-088-658-42	Sequence 42, Appl	368	20	0.4	65	3	US-09-351-029-6	Sequence 6, Appl
296	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	369	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
297	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	370	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
298	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	371	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
299	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	372	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
300	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	373	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
301	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	374	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
302	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	375	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
303	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	376	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
304	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	377	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
305	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	378	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
306	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	379	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
307	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	380	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
308	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	381	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
309	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	382	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
310	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	383	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
311	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	384	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
312	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	385	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
313	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	386	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
314	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	387	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
315	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	388	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
316	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	389	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
317	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	390	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
318	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	391	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl
319	20.2	0.4	98	2	US-08-471-907A-42	Sequence 210, Appl	392	20	0.4	65	3	US-09-457-324-5	Sequence 5, Appl

539	19.4	0.4	68	5	PCT-US96-06060-197	Sequence 197, App	c 612	19.2	0.4	45	4	US-09-414-117-76	Sequence 76, App
540	19.4	0.4	70	1	US-08-090-193-41	Sequence 41, App	c 613	19.2	0.4	45	4	US-09-678-437-76	Sequence 76, App
541	19.4	0.4	70	2	US-08-488-031-41	Sequence 41, App	c 614	19.2	0.4	47	4	US-09-438-016-2	Sequence 2, App
542	19.4	0.4	70	2	US-08-486-569-41	Sequence 41, App	c 615	19.2	0.4	47	4	US-09-438-016-8	Sequence 8, App
543	19.4	0.4	70	2	US-08-488-027-41	Sequence 41, App	c 616	19.2	0.4	48	1	US-07-797-556-9	Sequence 9, App
544	19.4	0.4	70	2	US-08-090-192-40	Sequence 40, App	c 617	19.2	0.4	47	1	US-09-538-709-1005	Sequence 1005, App
545	19.4	0.4	70	2	US-08-482-663-41	Sequence 41, App	c 618	19.2	0.4	54	1	US-08-758-306-952	Sequence 952, App
546	19.4	0.4	70	3	US-08-482-658-41	Sequence 41, App	c 619	19.2	0.4	54	2	US-08-585-684B-2660	Sequence 2660, App
547	19.4	0.4	70	3	US-08-470-349-40	Sequence 40, App	c 620	19.2	0.4	54	4	US-09-038-073-2660	Sequence 2660, App
548	19.4	0.4	70	3	US-08-618-1008-31	Sequence 31, App	c 621	19.2	0.4	55	4	US-09-383-143-6	Sequence 6, App
549	19.4	0.4	70	3	US-08-475-610-41	Sequence 41, App	c 622	19.2	0.4	55	4	US-09-394-630-4	Sequence 4, App
550	19.4	0.4	70	3	US-09-275-850-144	Sequence 144, App	c 623	19.2	0.4	58	3	US-08-718-904-103	Sequence 103, App
551	19.4	0.4	70	4	PCT-US93-00277-41	Sequence 41, App	c 624	19.2	0.4	62	4	US-08-464-514-22	Sequence 22, App
552	19.4	0.4	70	5	PCT-US93-00278-40	Sequence 40, App	c 625	19.2	0.4	62	4	US-08-486-403-22	Sequence 22, App
553	19.4	0.4	71	1	US-08-802-824-4	Sequence 4, App	c 626	19.2	0.4	69	2	US-08-894-578-166	Sequence 166, App
554	19.4	0.4	71	2	US-08-802-824-4	Sequence 4, App	c 627	19.2	0.4	69	2	US-08-894-578-178	Sequence 178, App
555	19.4	0.4	71	2	US-09-057-537-4	Sequence 3, App	c 628	19.2	0.4	71	2	US-08-465-591A-68	Sequence 68, App
556	19.4	0.4	72	1	US-08-446-102-2	Sequence 3, App	c 629	19.2	0.4	71	2	US-08-465-594A-68	Sequence 253, App
557	19.4	0.4	75	2	US-08-549-211-2	Sequence 2, App	c 630	19.2	0.4	71	5	US-08-433-126A-34	Sequence 34, App
558	19.4	0.4	76	2	US-08-549-211-2	Sequence 3, App	c 631	19.2	0.4	72	1	US-08-433-126A-34	Sequence 34, App
559	19.4	0.4	78	1	US-07-927-316A-3	Sequence 6, App	c 632	19.2	0.4	72	1	US-08-976-413A-34	Sequence 27, App
560	19.4	0.4	78	1	US-08-459-263-6	Sequence 6, App	c 633	19.2	0.4	72	3	US-09-718-299-27	Sequence 27, App
561	19.4	0.4	78	1	US-08-459-263-6	Sequence 6, App	c 634	19.2	0.4	72	3	US-09-718-299-27	Sequence 27, App
562	19.4	0.4	80	4	US-09-461-697-378	Sequence 378, App	c 635	19.2	0.4	72	4	US-08-434-001-61	Sequence 61, App
563	19.4	0.4	80	4	US-07-832-905B-61	Sequence 61, App	c 636	19.2	0.4	72	5	PCT-US96-06059-34	Sequence 34, App
564	19.4	0.4	80	1	US-07-832-905B-62	Sequence 62, App	c 637	19.2	0.4	73	1	US-08-434-001-61	Sequence 61, App
565	19.4	0.4	80	2	US-08-700-757-61	Sequence 61, App	c 638	19.2	0.4	73	1	US-08-433-585-61	Sequence 61, App
566	19.4	0.4	81	1	US-08-238-863-22	Sequence 22, App	c 639	19.2	0.4	73	1	US-08-433-585-61	Sequence 61, App
567	19.4	0.4	81	1	US-08-238-863-22	Sequence 22, App	c 640	19.2	0.4	73	1	US-08-434-425-61	Sequence 61, App
568	19.4	0.4	81	1	US-07-756-251A-14	Sequence 14, App	c 641	19.2	0.4	73	1	US-08-434-425-61	Sequence 61, App
569	19.4	0.4	81	1	US-08-443-407-22	Sequence 22, App	c 642	19.2	0.4	73	1	US-08-437-667-61	Sequence 61, App
570	19.4	0.4	81	1	US-08-443-407-22	Sequence 22, App	c 643	19.2	0.4	73	2	US-08-437-667-61	Sequence 61, App
571	19.4	0.4	81	1	US-08-443-407-22	Sequence 22, App	c 644	19.2	0.4	73	2	US-08-437-667-61	Sequence 61, App
572	19.4	0.4	81	5	PCT-US95-05600-189	Sequence 189, App	c 645	19.2	0.4	73	3	US-08-906-955-61	Sequence 61, App
573	19.4	0.4	81	5	PCT-US95-05600-189	Sequence 189, App	c 646	19.2	0.4	73	3	US-08-906-955-61	Sequence 61, App
574	19.4	0.4	82	1	US-08-497-134A-19	Sequence 19, App	c 647	19.2	0.4	73	3	US-08-945-909-61	Sequence 61, App
575	19.4	0.4	82	1	US-08-481-658B-37	Sequence 37, App	c 648	19.2	0.4	73	3	US-08-945-909-61	Sequence 61, App
576	19.4	0.4	82	2	US-08-477-504A-37	Sequence 37, App	c 649	19.2	0.4	73	4	US-09-396-002A-61	Sequence 61, App
577	19.4	0.4	82	2	US-08-486-756A-37	Sequence 37, App	c 650	19.2	0.4	73	4	US-09-396-002A-61	Sequence 61, App
578	19.4	0.4	82	2	US-08-485-862B-37	Sequence 37, App	c 651	19.2	0.4	73	5	PCT-US96-06060-61	Sequence 61, App
579	19.4	0.4	82	3	US-08-787-739-37	Sequence 37, App	c 652	19.2	0.4	73	5	PCT-US96-06060-61	Sequence 61, App
580	19.4	0.4	82	3	US-08-487-077A-37	Sequence 37, App	c 653	19.2	0.4	74	4	US-09-025-769B-154	Sequence 154, App
581	19.4	0.4	82	3	US-08-485-863A-37	Sequence 37, App	c 654	19.2	0.4	81	1	US-08-238-863-16	Sequence 16, App
582	19.4	0.4	82	4	US-09-269-592-6	Sequence 6, App	c 655	19.2	0.4	81	1	US-08-443-407-16	Sequence 16, App
583	19.4	0.4	82	4	US-09-177-776-37	Sequence 37, App	c 656	19.2	0.4	81	1	US-08-443-407-16	Sequence 16, App
584	19.4	0.4	82	4	US-09-177-776-37	Sequence 37, App	c 657	19.2	0.4	81	2	US-08-233-012C-69	Sequence 69, App
585	19.4	0.4	84	3	US-08-383-753-96	Sequence 96, App	c 658	19.2	0.4	81	3	PCT-US95-05600-160	Sequence 160, App
586	19.4	0.4	85	1	US-08-586-772-96	Sequence 96, App	c 659	19.2	0.4	83	3	US-08-783-853A-82	Sequence 82, App
587	19.4	0.4	85	2	US-08-586-772-96	Sequence 96, App	c 660	19.2	0.4	83	3	US-08-783-853A-82	Sequence 82, App
588	19.4	0.4	85	2	US-09-512-983-96	Sequence 96, App	c 661	19.2	0.4	86	3	US-09-344-050-82	Sequence 82, App
589	19.4	0.4	85	4	US-09-364-543-88	Sequence 88, App	c 662	19.2	0.4	86	4	US-08-637-759B-1	Sequence 1, App
590	19.4	0.4	85	4	US-09-364-543-88	Sequence 88, App	c 663	19.2	0.4	89	3	US-08-637-759B-1	Sequence 1, App
591	19.4	0.4	88	3	US-08-836-561-95	Sequence 95, App	c 664	19.2	0.4	89	4	US-08-871-355A-1	Sequence 1, App
592	19.4	0.4	88	3	US-08-836-561-95	Sequence 95, App	c 665	19.2	0.4	89	4	US-08-871-355A-1	Sequence 1, App
593	19.4	0.4	88	3	US-07-964-624D-32	Sequence 32, App	c 666	19.2	0.4	89	4	US-08-871-355A-1	Sequence 1, App
594	19.4	0.4	89	1	US-08-442-062-32	Sequence 32, App	c 667	19.2	0.4	90	2	US-08-769-967A-74	Sequence 74, App
595	19.4	0.4	89	1	US-08-442-062-32	Sequence 32, App	c 668	19.2	0.4	90	2	US-08-769-967A-74	Sequence 74, App
596	19.4	0.4	89	3	US-08-959-853-10	Sequence 10, App	c 669	19.2	0.4	91	3	US-08-974-549A-702	Sequence 702, App
597	19.4	0.4	89	3	US-09-165-616-32	Sequence 32, App	c 670	19.2	0.4	91	3	US-08-974-549A-702	Sequence 702, App
598	19.4	0.4	93	2	US-08-592-383-8	Sequence 8, App	c 671	19.2	0.4	92	4	US-09-344-050-16	Sequence 16, App
599	19.4	0.4	93	2	US-08-467-963C-34	Sequence 34, App	c 672	19.2	0.4	92	4	US-09-344-050-16	Sequence 16, App
600	19.4	0.4	98	2	US-08-838-189D-34	Sequence 34, App	c 673	19.2	0.4	93	2	US-08-836-561-84	Sequence 84, App
601	19.4	0.4	98	2	US-08-838-189D-34	Sequence 34, App	c 674	19.2	0.4	93	2	US-08-836-561-84	Sequence 84, App
602	19.4	0.4	98	3	US-08-834-639E-34	Sequence 34, App	c 675	19.2	0.4	97	1	US-08-976-413A-116	Sequence 116, App
603	19.4	0.4	98	3	US-08-834-639E-34	Sequence 34, App	c 676	19.2	0.4	97	1	US-08-976-413A-116	Sequence 116, App
604	19.4	0.4	98	4	US-08-145-705A-16	Sequence 16, App	c 677	19.2	0.4	97	1	US-08-976-413A-116	Sequence 116, App
605	19.4	0.4	100	3	US-08-836-561-84	Sequence 16, App	c 678	19.2	0.4	100	1	US-07-797-556-7	Sequence 7, App
606	19.4	0.4	100	3	US-08-269-592-16	Sequence 16, App	c 679	19.2	0.4	100	1	US-07-797-556-7	Sequence 7, App
607	19.4	0.4	100	3	US-08-269-592-16	Sequence 16, App	c 680	19.2	0.4	100	1	US-08-217-210B-7	Sequence 7, App
608	19.2	0.4	34	4	US-08-486-403-19	Sequence 19, App	c 681	19.2	0.4	100	4	US-09-298-886-15	Sequence 15, App
609	19.2	0.4	34	4	US-08-486-403-19	Sequence 19, App	c 682	19.2	0.4	100	4	US-09-298-886-15	Sequence 15, App
610	19.2	0.4	45	2	US-08-830-048-76	Sequence 76, App	c 683	19.2	0.4	42	3	US-08-334-847-730	Sequence 730, App
611	19.2	0.4	45	2	US-08-830-048-76	Sequence 76, App	c 684	19.2	0.4	42	3	US-08-334-847-730	Sequence 730, App

C 685	19	0.4	42	4	US-09-569-344-28	Sequence 28, App1	C 758	19	0.4	71	4	US-09-364-902-27	Sequence 27, App1
C 686	19	0.4	47	2	US-08-621-803-244	Sequence 244, App	C 759	19	0.4	72	3	US-08-506-553-15	Sequence 15, App1
C 687	19	0.4	48	4	US-09-217-352-244	Sequence 244, App	C 760	19	0.4	73	1	US-08-567-047-7	Sequence 7, App1
C 688	19	0.4	48	1	US-08-317-102-2	Sequence 2, App1	C 761	19	0.4	73	1	US-08-567-047-8	Sequence 8, App1
C 689	19	0.4	49	4	US-08-706-945D-99	Sequence 99, App1	C 762	19	0.4	73	2	US-08-567-048-7	Sequence 7, App1
C 690	19	0.4	50	1	US-08-171-389-587	Sequence 587, App	C 763	19	0.4	73	2	US-08-567-048-8	Sequence 8, App1
C 691	19	0.4	50	1	US-08-123-936-587	Sequence 587, App	C 764	19	0.4	73	2	US-09-502-558-34	Sequence 34, App1
C 692	19	0.4	50	2	US-08-475-228A-587	Sequence 587, App	C 765	19	0.4	78	1	US-08-446-102-1	Sequence 1, App1
C 693	19	0.4	50	3	US-08-482-080A-587	Sequence 587, App	C 766	19	0.4	78	1	US-08-446-102-2	Sequence 2, App1
C 694	19	0.4	50	4	US-09-354-947-587	Sequence 587, App	C 767	19	0.4	78	1	US-08-447-169A-87	Sequence 87, App1
C 695	19	0.4	50	5	PCT-US93-12388-567	Sequence 587, App	C 768	19	0.4	78	2	US-08-233-012C-87	Sequence 87, App1
C 696	19	0.4	52	1	US-08-171-389-238	Sequence 238, App	C 769	19	0.4	78	4	US-08-617-010C-15	Sequence 15, App1
C 697	19	0.4	52	1	US-08-530-492-123	Sequence 123, App	C 770	19	0.4	78	4	US-09-566-591-15	Sequence 15, App1
C 698	19	0.4	52	2	US-08-123-936-238	Sequence 238, App	C 771	19	0.4	78	4	US-08-744-481A-25	Sequence 25, App1
C 699	19	0.4	52	2	US-08-475-228A-238	Sequence 238, App	C 772	19	0.4	79	4	US-08-839-624-8	Sequence 8, App1
C 700	19	0.4	52	3	US-08-482-080A-238	Sequence 238, App	C 773	19	0.4	79	4	US-09-150-812-8	Sequence 8, App1
C 701	19	0.4	52	4	US-08-906-517-123	Sequence 123, App	C 774	19	0.4	80	1	US-08-595-226B-4	Sequence 4, App1
C 702	19	0.4	52	4	US-09-143-634-27	Sequence 27, App1	C 775	19	0.4	80	2	US-08-906-491-4	Sequence 8, App1
C 703	19	0.4	52	4	US-09-354-947-238	Sequence 238, App	C 776	19	0.4	80	3	US-08-513-968-52	Sequence 52, App1
C 704	19	0.4	52	5	PCT-US93-12388-238	Sequence 238, App	C 777	19	0.4	80	3	US-08-513-968-52	Sequence 52, App1
C 705	19	0.4	53	4	US-09-091-814-28	Sequence 28, App1	C 778	19	0.4	80	3	US-08-506-553C-16	Sequence 16, App1
C 706	19	0.4	53	4	US-09-091-814-28	Sequence 28, App1	C 779	19	0.4	80	4	US-09-188-214-4	Sequence 4, App1
C 707	19	0.4	54	4	US-08-584-040-8241	Sequence 8241, App	C 780	19	0.4	80	4	US-09-188-214-4	Sequence 4, App1
C 708	19	0.4	54	4	US-08-741-881-81	Sequence 8241, App	C 781	19	0.4	80	4	US-09-149-727-59	Sequence 59, App1
C 709	19	0.4	57	1	US-08-739-158-81	Sequence 81, App1	C 782	19	0.4	80	4	US-08-839-624-8	Sequence 8, App1
C 710	19	0.4	57	1	US-08-739-158-81	Sequence 81, App1	C 783	19	0.4	81	1	US-08-238-863-71	Sequence 71, App1
C 711	19	0.4	57	2	US-08-596-387B-49	Sequence 49, App1	C 784	19	0.4	81	1	US-08-318-107-11	Sequence 11, App1
C 712	19	0.4	57	2	US-08-404-796-81	Sequence 81, App1	C 785	19	0.4	81	1	US-08-443-407-71	Sequence 71, App1
C 713	19	0.4	57	3	US-08-931-869-81	Sequence 81, App1	C 786	19	0.4	81	2	US-08-332-562A-10	Sequence 10, App1
C 714	19	0.4	57	3	US-09-067-615-49	Sequence 49, App1	C 787	19	0.4	81	4	US-08-839-624-32	Sequence 32, App1
C 715	19	0.4	57	4	US-09-350-399-81	Sequence 81, App1	C 788	19	0.4	81	4	US-08-556-828B-90	Sequence 90, App1
C 716	19	0.4	57	4	US-09-350-399-81	Sequence 81, App1	C 789	19	0.4	81	4	US-08-470-953A-8	Sequence 8, App1
C 717	19	0.4	57	5	PCT-US95-09816A-49	Sequence 49, App1	C 790	19	0.4	81	4	US-08-470-953A-8	Sequence 8, App1
C 718	19	0.4	58	1	US-08-171-389-25	Sequence 25, App1	C 791	19	0.4	81	5	PCT-US95-05600-215	Sequence 215, App1
C 719	19	0.4	58	1	US-08-123-936-25	Sequence 25, App1	C 792	19	0.4	81	5	US-09-150-812-32	Sequence 32, App1
C 720	19	0.4	58	1	US-08-625-691-31	Sequence 31, App1	C 793	19	0.4	82	6	US-09-149-727-71	Sequence 71, App1
C 721	19	0.4	58	2	US-08-475-228A-25	Sequence 25, App1	C 794	19	0.4	82	6	US-08-976-413A-253	Sequence 253, App1
C 722	19	0.4	58	3	US-08-482-080A-25	Sequence 25, App1	C 795	19	0.4	83	3	US-07-964-624D-45	Sequence 45, App1
C 723	19	0.4	58	4	US-09-387-699-16	Sequence 16, App1	C 796	19	0.4	84	1	US-08-442-062-45	Sequence 45, App1
C 724	19	0.4	58	4	US-09-140-201-6	Sequence 6, App1	C 797	19	0.4	84	1	US-08-467-965C-11	Sequence 11, App1
C 725	19	0.4	58	4	US-09-354-947-25	Sequence 25, App1	C 798	19	0.4	84	1	US-08-467-965C-11	Sequence 11, App1
C 726	19	0.4	58	4	US-09-641-259B-16	Sequence 16, App1	C 799	19	0.4	85	4	US-08-839-624-31	Sequence 31, App1
C 727	19	0.4	58	4	PCT-US93-12388-25	Sequence 25, App1	C 800	19	0.4	85	4	US-08-839-624-31	Sequence 31, App1
C 728	19	0.4	58	5	PCT-US93-12388-25	Sequence 25, App1	C 801	19	0.4	86	4	US-08-467-965A-11	Sequence 11, App1
C 729	19	0.4	60	4	US-09-116-032-16	Sequence 16, App1	C 802	19	0.4	86	4	US-08-467-965A-11	Sequence 11, App1
C 730	19	0.4	60	4	US-09-626-929-14	Sequence 14, App1	C 803	19	0.4	86	4	US-08-467-965A-11	Sequence 11, App1
C 731	19	0.4	60	4	US-09-484-850-14	Sequence 14, App1	C 804	19	0.4	86	2	US-08-838-189D-11	Sequence 11, App1
C 732	19	0.4	60	4	US-09-408-932-14	Sequence 14, App1	C 805	19	0.4	86	2	US-08-838-189D-11	Sequence 11, App1
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C 749	19	0.4	68	2	US-08-179-557-28	Sequence 28, App1	C 822	19	0.4	87	5	PCT-US96-06059-72	Sequence 72, App1
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C 752	19	0.4	70	1	US-08-487-141B-107	Sequence 107, App	C 825	19	0.4	88	3	US-08-836-561-90	Sequence 90, App1
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858	18.8	0.4	39	2	US-08-910-731-14	Sequence 14, Appl	C 931	18.8	0.4	83	4	US-09-603-658-39	Sequence 39, Appl
859	18.8	0.4	39	3	US-08-713-815A-6	Sequence 6, Appl1	C 932	18.8	0.4	83	5	US-09-603-658-39	Sequence 39, Appl
860	18.8	0.4	40	2	US-08-683-743-9	Sequence 9, Appl1	C 933	18.8	0.4	84	4	US-08-687-080-58	Sequence 58, Appl
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C 977 18.8 0.4 91 2 US-08-646-360-140 Sequence 140, App
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C 987 18.8 0.4 95 1 US-08-458-101-376 Sequence 12, Appl
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C 994 18.8 0.4 98 1 US-08-654-737B-5 Sequence 133, App
C 995 18.8 0.4 99 4 US-09-513-783A-133 Sequence 91, Appl
996 18.8 0.4 100 1 US-08-129-930B-91 Sequence 46, Appl
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998 18.8 0.4 100 4 US-09-242-690A-57 Sequence 91, Appl
1000 18.8 0.4 100 4 US-08-976-288A-91

ALIGNMENTS

RESULT 1
US-08-400-256-4/C
Sequence 4, Application US/08400256
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TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESSES:

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COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-400-256-4

Query Match 0.5%; Score 26; DB 1; Length 100;
Best Local Similarity 55.6%; Pred. No. 7.6e+02;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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DB 97 AAGTGTGACGACGCTAAGGATATGCTGGAACAATGTGTACTTATCTGTCTTGTAC 38
QY 4529 TATTACATTAAGACTGTGCTGAGACGAG 4558
DB 37 CAATTGGAATACTACTGTGTAGACGAG 8

RESULT 2

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Sequence 4, Application US/08975365
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TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESSES:

ADDRESSEE: No. 60110070 No. 6011007disk of No. 6011007th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,365
FILING DATE:
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985,220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-975-365-4

Query Match 0.5%; Score 26; DB 3; Length 100;
Best Local Similarity 55.6%; Pred. No. 7.6e+02;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 4469 AAGATGAGCGCTAGTAAATATGACTTGGAATTTCTTAATCACTAGTATGTA 4528
DB 97 AAGTGTGACGACGCTAAGGATATGCTGGAACAATGTGTACTTATCTGTCTTGTAC 38
QY 4529 TATTACATTAAGACTGTGCTGAGACGAG 4558
DB 37 CAATTGGAATACTACTGTGTAGACGAG 8

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RESULT 3
US-08-427-097-5
Sequence 5, Application US/08427097
Patent No. 5668294
GENERAL INFORMATION:
APPLICANT: Meagher, Richard B.
APPLICANT: Sommers, Anne O.
TITLE OF INVENTION: Metal Resistance Sequences and
TITLE OF INVENTION: Transgenic Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
ZIP: 80303
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,097
FILING DATE: 21-APR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 40-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-427-097-5

Query Match
Best Local Similarity 54.3%; Score 25.2; DB 1; Length 99;
Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 3026 ATGTCTGACTAATGATGAGTGTAGAGGTACAGACCCAGCTGGCGACTCAAGCAT 3085
DB 2 AAGACCCAGCTATAGTGAAGCTGTACTGCTGCATTCGATGAGGCAATGAGTGC 61
QY 3086 TTGATTTTCTACAGCAATTTGACCTGCTTAT 3119
DB 62 GTGAGCATCTACAGCAAGCCAGTTGCTTAT 95

RESULT 4
US-08-878-957-5
Sequence 5, Application US/08878957
Patent No. 5965796
GENERAL INFORMATION:
APPLICANT: Meagher, Richard B.
APPLICANT: Sommers, Anne O.
TITLE OF INVENTION: Metal Resistance Sequences and
TITLE OF INVENTION: Transgenic Plants
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
```

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STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,957
FILING DATE: 19-JUN-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/427,097
FILING DATE: 21-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 40-94A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-878-957-5

Query Match
Best Local Similarity 54.3%; Score 25.2; DB 2; Length 99;
Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 3026 ATGTCTGACTAATGATGAGTGTAGAGGTACAGACCCAGCTGGCGACTCAAGCAT 3085
DB 2 AAGACCCAGCTATAGTGAAGCTGTACTGCTGCATTCGATGAGGCAATGAGTGC 61
QY 3086 TTGATTTTCTACAGCAATTTGACCTGCTTAT 3119
DB 62 GTGAGCATCTACAGCAAGCCAGTTGCTTAT 95

RESULT 5
US-09-641-638-918/C
Sequence 918, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bouquelieret, Lydie
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
FILE REFERENCE: GENSET.051CE1
CURRENT APPLICATION NUMBER: US/09/641,638
FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 918
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

TOPOLOGY: linear
 MOLECULE TYPE: DNA
 -08-458-424B-78

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Query Match      0.5%;      Score 24.6;  DB 1;      Length 71;
Best Local Similarity 65.5%;  Pred. No. 1.5e+03;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0
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Query Match	0.58;	Score 24.6;	DB 4;	Length 71;
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? FILING DATE: 20 MARCH 1990
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Barry J. Swanson
 ? REGISTRATION NUMBER: 33,215
 ? REFERENCE/DOCKET NUMBER:
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (303) 793-3333
 ? TELEFAX: (303) 793-3433
 ? INFORMATION FOR SEQ. ID NOS: 78:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 71 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA
 ?
 PCT-US96-08014-78

Query Match 0.5%; Score 24.6; DB 5; Length 71;
Best Local Similarity 65.5%; Pred. No. 1.5e+03;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 3958 GAACATGATAGTATGCTATATCAACACATCCATTCGATCAAGTCTCC 4012
DB 56 GAACACGTAAGTATAGTATATTAACAACATCCCTGCGCATCTGCTCC 2

RESULT 10

US-09-100-664A-5
Sequence 5, Application US/09100664A
Patent No. 6057129

GENERAL INFORMATION:

APPLICANT: YOUNG, MICHAEL W.
APPLICANT: KLOSS, BRIAN
APPLICANT: BLAU, JUSTIN
APPLICANT: PRICE, JEFFREY
TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,664A
FILING DATE: 19-JUN-1998
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULAR TYPE: CDNA
HYPOTHETICAL: NO
US-09-100-664A-5

Query Match 0.5%; Score 24.6; DB 3; Length 72;
Best Local Similarity 59.2%; Pred. No. 1.6e+03;
Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

OY 3694 ATTGGAAGAGCCAGTATGGAAGGCTGTACACCTGCATCACCGCGGAGACTG 3753
DB 1 ATAGATCGGATCGTTCGGCGACATCTACCTGGGACACGATCAACACTCTGGAGAG 60
OY 3754 ATGGCCATGAA 3764
DB 61 GTGGCATCAA 71

RESULT 11
US-09-335-983-5
Sequence 5, Application US/09335983
Patent No. 6436628
GENERAL INFORMATION:

APPLICANT: Young, Michael W
APPLICANT: Kloss, Brian
APPLICANT: Blau, Justin
APPLICANT: Price, Jeffrey

TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE THEREOF
FILE REFERENCE: 600-1-221N
CURRENT APPLICATION NUMBER: US/09/335,983
EARLIER FILING DATE: 1999-06-18
EARLIER APPLICATION NUMBER: 09/100,664
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 5
LENGTH: 72
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-335-983-5

Query Match 0.5%; Score 24.6; DB 4; Length 72;
Best Local Similarity 59.2%; Pred. No. 1.6e+03;
Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

OY 3694 ATTGGAAGAGCCAGTATGGAAGGCTGTACACCTGCATCACCGCGGAGACTG 3753
DB 1 ATAGATCGGATCGTTCGGCGACATCTACCTGGGACACGATCAACACTCTGGAGAG 60
OY 3754 ATGGCCATGAA 3764
DB 61 GTGGCATCAA 71

RESULT 12

US-09-506-729-21/c
Sequence 21, Application US/09506729
Patent No. 6365352

GENERAL INFORMATION:

APPLICANT: Yerramilli, Subrahmanyam V.
APPLICANT: Prashar, Yatindra
APPLICANT: Newberger, Peter
APPLICANT: Gouen, Jon
TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
FILE REFERENCE: 44921-5016-US
CURRENT APPLICATION NUMBER: US/09/506,729
EARLIER FILING DATE: 2000-02-18
EARLIER APPLICATION NUMBER: PCT/US98/17284
EARLIER FILING DATE: 1998-08-21
EARLIER APPLICATION NUMBER: 60/056,844
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 21
LENGTH: 98
TYPE: DNA
ORGANISM: Homo sapiens
US-09-506-729-21

Query Match 0.5%; Score 24.6; DB 4; Length 98;
Best Local Similarity 59.2%; Pred. No. 1.9e+03;
Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

OY 4911 GTTGTATGCAAAAGGCTGATGTAAGAAATTAAGAAAAGGCTCTTTTCAATTAAT 4970
DB 93 GTTATCATACATAAGACCGCATGCTATATATACAAAGGGGGTCTTTTTCATTATTAAC 34
OY 4971 GGTATATTTTA 4981
DB 33 GTTACAAATATA 23

RESULT 13
US-08-400-256-9/c


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ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,365
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lambirth, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985.220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-975-365-9

Query Match
Post Local Similarity 0.5%; Score 24.4; DB 3; Length 100;
Matches 49; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

OY 4469 AAGAAATGACAGCTACTAGACATATAGATGACTTGGAAAAATTCCTTAATCAGCTAGTATGTAA 4528
DB 97 AAGTCGACGACGCGTAAGGCGTATCGTTGACACAAATGCTGACTTCTATCTGTCTTTTATAC 38
OY 4529 TATTTACATTAAGACTGCTCGAAGACGAG 4558
DB 37 CAATTGGAAACTACTGTGTTAGACGCGAG 8

RESULT 15
US-08-182-175A-54
; Sequence 54, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamelly Floyd

```

REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: E. COLI
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 92-2
FEATURE:
NAME/KEY: CDS
LOCATION: 2..88
OTHER INFORMATION: /function="synthetic storage protein"
OTHER INFORMATION: /product="protein"
OTHER INFORMATION: /gene="ssp"
OTHER INFORMATION: /standard_name="5.11.11.5"
US-08-182-175A-54

Query Match
Best Local Similarity 0.5%; Score 24; DB 1; Length 97;
Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1120 GAGTATGAGGCGTATGACACAGAGAGATTAAGAGAGTTGGAAGTGTACGATGAG 1179
DB 10 GAGATGAGGCGGATGAGAGAGATGAAGTGTGATGAGAGAGATGAAGTGTGATGA 69
QY 1180 AGTGAAGAGAA 1191
DB 70 AGAGAGATGAA 81

RESULT 16
US-08-474-633A-63
Sequence 63, Application US/08474633A
Patent No. 5773691
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE
TITLE OF INVENTION: INCREASING THE LYSINE
TITLE OF INVENTION: AND THREONINE CONTENT
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESS: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. STEGELL
REGISTRATION NUMBER: 30,684

REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: E. COLI
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 92-2
FEATURE:
NAME/KEY: CDS
LOCATION: 2..88
OTHER INFORMATION: /function="synthetic storage protein"
OTHER INFORMATION: /product="protein"
OTHER INFORMATION: /gene="ssp"
OTHER INFORMATION: /standard_name="5.11.11.5"
US-08-474-633A-63

Query Match
Best Local Similarity 0.5%; Score 24; DB 1; Length 97;
Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1120 GAGTATGAGGCGTATGACACAGAGAGATTAAGAGAGTTGGAAGTGTACGATGAG 1179
DB 10 GAGATGAGGCGGATGAGAGAGATGAAGTGTGATGAGAGAGATGAAGTGTGATGA 69
QY 1180 AGTGAAGAGAA 1191
DB 70 AGAGAGATGAA 81

RESULT 17
US-08-823-771-63
Sequence 63, Application US/08823771
Patent No. 6459019
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING
TITLE OF INVENTION: INCREASING THE LYSINE
TITLE OF INVENTION: AND THREONINE CONTENT
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESS: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. STEGELL
REGISTRATION NUMBER: 30,684
FILING DATE: <Unknown>

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Page 15

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ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. STEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: E. coli
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 92-2
FEATURE:
NAME/KEY: CDS /function= "synthetic
LOCATION: 2..88 /product= "protein"
OTHER INFORMATION:
storage protein
/ gene= "asp"
/standard.name=
"5.11.11.5"
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-08-823-771-63
Query Match 0.5%; Score 24; DB 4; Length 97;
Best Local Similarity 58.3%; Pred. No. 2.7e+03;
Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
OY 1120 GAGTATGAGGCGTATGACACAGAGAGATTAAGAGCTTGAGAGAGTACGATGAG 1179
DB 10 GAAGATGAGGCGGAGAGAGAGATGAGTGTGAGAGAGAGATGAGATGATGAG 69
OY 1180 AGTGAAGAGAA 1191
DB 70 AGAGAGAGATGAA 81
RESULT 18
PCT-US92-06412-54
Sequence 54, Application PC/7US9206412
GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA: PCT/US92/06412
APPLICATION NUMBER: 530
CLASSIFICATION: 530
PRIORITY APPLICATION DATA: 07/743,006
APPLICATION NUMBER: 9 August 1991
FILING DATE: 9 August 1991
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ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: E. coli
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 92-2
FEATURE:
NAME/KEY: CDS /function= "synthetic storage protein
LOCATION: 2..88 /product= "protein"
OTHER INFORMATION:
storage protein
/ gene= "ssp"
/standard.name= "5.11.11.5"
PCT-US92-06412-54
Query Match 0.5%; Score 24; DB 5; Length 97;
Best Local Similarity 58.3%; Pred. No. 2.7e+03;
Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
OY 1120 GAGTATGAGGCGTATGACACAGAGAGATTAAGAGCTTGAGAGAGTACGATGAG 1179
DB 10 GAAGATGAGGCGGAGAGAGAGATGAGTGTGAGAGAGAGATGAGATGATGAG 69
OY 1180 AGTGAAGAGAA 1191
DB 70 AGAGAGAGATGAA 81
RESULT 19
US-08-672-158A-8
Sequence 8, Application US/08672158A
GENERAL INFORMATION:
APPLICANT: Sheryl Thompson
TITLE OF INVENTION: Modification of Cryptic Splice Sites In
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57703710 No. 57703710disk of No. 57703711th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,158A
FILING DATE: 27-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agis D., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 4855,000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
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US-08-123-702-21/c
Sequence 21, Application US/08123702
Patent No. 5604131
GENERAL INFORMATION:
APPLICANT: Wadsworth, Samuel
APPLICANT: Snyder, Benjamin
APPLICANT: Reddy, Vernur, B.
APPLICANT: Wei, Chamer
TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding Ape770
Patent No. 5604131
TITLE OF INVENTION: Containing a Genomic DNA Insert of the KI and OX-2 Regions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,702
FILING DATE: 17-SEPT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: TS1121
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-123-702-21
Query Match 0.4%; Score 22.4; DB 1; Length 90;
Best Local Similarity 55.0%; Pred. No. 7.4e+03; Mismatches 36; Indels 0; Gaps 0;
Matches 44; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
OY 315 ATCTTGGCAAAATATCATTCAGATGTGATCTCATATAGCCTTACCTGAGCCTTGG 374
DB 82 ATCTAACCAACAAACATCTCTTGTGAGTACACACATCAGACGACGACGAG 23
OY 375 CTGTAGCATGCTAGCTTC 394
DB 22 CAGCAGCCACCATTTACTTC 3
RESULT 29
US-08-332-766A-41
Sequence 41, Application US/08332766A
Patent No. 5643647
GENERAL INFORMATION:
APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.

ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-332-766A-41
Query Match 0.4%; Score 22.4; DB 2; Length 95;
Best Local Similarity 55.0%; Pred. No. 7.6e+03; Mismatches 36; Indels 0; Gaps 0;
Matches 44; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
OY 139 AAGAGAAATGATGACCAATTCAGCTTCACATTAAGACACCTGAGAAACAGTGAGAG 198
DB 1 AAGAGAGAAATGATGACCAATTCAGCTTCACATTAAGACACCTGAGAAACAGTGAGAG 60
OY 199 AATGTGAAGATATACGCTA 218
DB 61 GAGGTGGAAAAAACACACTA 80
RESULT 30
US-08-182-175A-48
Sequence 48, Application US/08182175A
Patent No. 5559223
GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
FILING DATE: 800
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:


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1  NAME: Linda Axamethy Floyd
2  REGISTRATION NUMBER: 33,652
3  REFERENCE/POCKET NUMBER: BB-1031
4  TELECOMMUNICATION INFORMATION:
5  TELEPHONE: (302) 992-4929
6  TELEFAX: (302) 892-7949
7  TELEX: 835420
8  INFORMATION FOR SEQ ID NO: 48:
9  SEQUENCE CHARACTERISTICS:
10 LENGTH: 97 base pairs
11 TYPE: nucleic acid
12 STRANDEDNESS: double
13 TOPOLOGY: linear
14 MOLECULE TYPE: linear
15 ORIGINAL SOURCE:
16 STRAIN: E. coli
17 CELL TYPE: DH5 alpha
18 IMMEDIATE SOURCE:
19 CLONE: 86-H23
20 FEATURE:
21 NAME/KEY: CDS
22 LOCATION: 2..88
23 OTHER INFORMATION:
24 OTHER INFORMATION:
25 OTHER INFORMATION:
26 OTHER INFORMATION:
27 /function= "synthetic storage protein"
28 /product= "protein"
29 /gene= "ssp"
30 /standard_name= "5.8.8.5"
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32 OS-08-182-175a-48

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Query Match	0.4%;	Score 22.4;	DB 1;	Length 97;
Best Local Similarity	56.9%;	Pred. No. 7.7e+03;		
Matches 41; Conservative	0;	Mismatches 31;		Indels

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QY	1120 GAGATGAGGGGTGATCACACGAAGAATAAAGAGCTTGCAAACTACTACCGATGAG	1179			
Dd	10 GAGATGAGGGGTGATGAGGAGAACCTGAAGATGAGAGAGAACTGCAAGAATGGA	69			
QY	1180 AGTGAAGAAGAA	1191			
Dd	70 AGAGAAGATGAA	81			

RESULT 31
US-08-474-633A-57
; Sequence 57, Application US/08474633A
; Patent No. 5773691

1 APPLICANT: E. I. DU PONT DE NEMOURS AND
2 COMPANY:
3 TITLE OF INVENTION: CHIMERIC GENES AND
4 METHODS FOR INCREASING
5 TITLE OF INVENTION: INCREASING THE LYSINE
6 TITLE OF INVENTION: AND THEORININE CONTENT
7 TITLE OF INVENTION: OF THE SEEDS OF PLANTS
8 NUMBER OF SEQUENCES: 107
9
10 CORRESPONDENCE ADDRESS:
11

ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESS: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19808

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.00C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL

```

1 REGISTRATION NUMBER: 30,684
2 REFERENCE/DOCKET NUMBER: BB-1037-C
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: 302-992-4931
5 TELEFAX: 302-773-0164
6
7 TELEX: 833420
8
9 INFORMATION FOR SEQ ID NO: 57:
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11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 97 base pairs
13 TYPE: nucleic acid
14 STRANDEDNESS: double
15 TOPOLOGY: linear
16
17 MOLECULE TYPE: linear
18
19 ORIGINAL SOURCE:
20 STRAIN: E. coli
21 CELL TYPE: DH5 alpha
22 IMMEDIATE SOURCE:
23 CLONE: 86-H23
24
25 FEATURE:
26
27 NAME/KEY: CDS
28 LOCATION: 2..88
29
30 OTHER INFORMATION:
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32 OTHER INFORMATION:
33 OTHER INFORMATION:
34 OTHER INFORMATION:
35 OTHER INFORMATION:
36 OTHER INFORMATION:
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38 /function= "synthetic
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40 /product= "protein"
41 /gene= "ssp"
42 /standard_name=
43 "5.8.8.5"
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45 US-08-474-633A-57

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US-08-474-633A-57

Query Match	0.48;	Score 22.4;	DB 1;	Length 97;
Best Local Similarity	56.9%;	Pred. No. 7.7e+03;		
Matches 41;	Conservative 0;	Mismatches 31;		Indels

QY	1120	GAGTATGAGGCGTGATGCACAGAAAGCAATTAAGAGCTTGAAACTACTACAGATGAC	1179
Db	10	GAAGATGGAAGCGCCATTGAGAGAACCTGAAGAGATGGAGAGAAAGCTGAAGAAGATGCA	69
QY	1180	AGTGAAGAAGAA	1191
Db	70	AGAGAAGATGAA	81

RESULT 32
US-08-823-771-57
Sequence 57, Application US/08823771
Patent No 6459019

GENERAL INFORMATION:

APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY

TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY

STREET: 1007 MARKET STREET
CITY: WILMINGTON

STATE: DELAWARE
COUNTRY: U.S.A.

COUNTRY: U
ZIP: 19898
GOVERNMENT: B

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS

SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/823,771

CLASSIFICATION: <U>
FILING DATE: 24-Mar-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633

APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McCleard
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX 39-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-465-594A-75

Query Match 0.4%; Score 22.2; DB 2; Length 71;
Best Local Similarity 56.9%; Pred. No. 7.3e+03;
Matches 29; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 31 GAGATCTTTATGACTCTCCGCCGACACCTCGACAGATGAACGC 81
DB 17 GACUATCUGGCGUCCAUCCACCCGAGCCGCGCGACGACUCCG 67

RESULT 35
US-08-465-594A-75
Sequence 75, Application US/08465594A
Patent No. 5846713
GENERAL INFORMATION:
APPLICANT: NIKOS PAGRATIS
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY HKPE NUCLEIC
TITLE OF INVENTION: ACID LIGANDS AND INHIBITORS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,594A
FILING DATE: 5-June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX 39-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-465-594A-75

Query Match 0.4%; Score 22.2; DB 2; Length 71;
Best Local Similarity 56.9%; Pred. No. 7.3e+03;
Matches 29; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 31 GAGATCTTTATGACTCTCCGCCGACACCTCGACAGATGAACGC 81
DB 17 GACUATCUGGCGUCCAUCCACCCGAGCCGCGCGACGACUCCG 67

RESULT 36
US-08-973-124-260
Sequence 260, Application US/08973124
Patent No. 6207816
GENERAL INFORMATION:
APPLICANT: LARRY GOLD et al.
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO GROWTH
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,124
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE: 30-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,594
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,783
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996

REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX36-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: All C's are 2'-F modified
FEATURE:
OTHER INFORMATION: All U's are 2'-F modified
US-08-488-402A-99

Query Match 0.4%; Score 22.2; DB 2; Length 85;
Best Local Similarity 64.7%; Pred. No. 8.1e+03;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 1280 TTGAGAGCTCGATCTGAGATGATCTCTTGGCTGGGAGACACAGACT 1330
DB 80 TTGTGAGCCTCCTGTCGAAGATCGTTCATTGACTAGGACCGTTAGGCT 30

RESULT 39
US-08-484-552A-99/c
Sequence 99, Application US/08484552A
Patent No. 5849890
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
APPLICANT: JAYASENA, SUMEDHA
APPLICANT: NIEUWLANDT, DAN
APPLICANT: DAVIS, KEN
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE LIGANDS TO CHORIONIC
TITLE OF INVENTION: GONADOTROPIN HORMONE AND RELATED GLYCOPROTEIN HORMONES
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,552A
FILING DATE: 07 JUNE 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,991
FILING DATE: 8-SEPTEMBER-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX36-2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: All C's are 2'-F modified
FEATURE:
OTHER INFORMATION: All U's are 2'-F modified
US-08-484-552A-99

Query Match 0.4%; Score 22.2; DB 2; Length 85;
Best Local Similarity 64.7%; Pred. No. 8.1e+03;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 1280 TTGAGAGCTCGATCTGAGATGATCTCTTGGCTGGGAGACACAGACT 1330
DB 80 TTGTGAGCCTCCTGTCGAAGATCGTTCATTGACTAGGACCGTTAGGCT 30

RESULT 40
PCT-US96-09472-99/c
Sequence 99, Application PC/TUS9609472
GENERAL INFORMATION:
APPLICANT: GOLD ET AL.
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO CHORIONIC GONADOTROPIN HORMONE AND RELATED
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09472
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/488,402
APPLICATION NUMBER:
FILING DATE: 07 JUNE 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,552
FILING DATE: 07 JUNE 1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX36-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: All C's are 2'-F modified
FEATURE:
OTHER INFORMATION: All U's are 2'-F modified
PCT-US96-09472-99

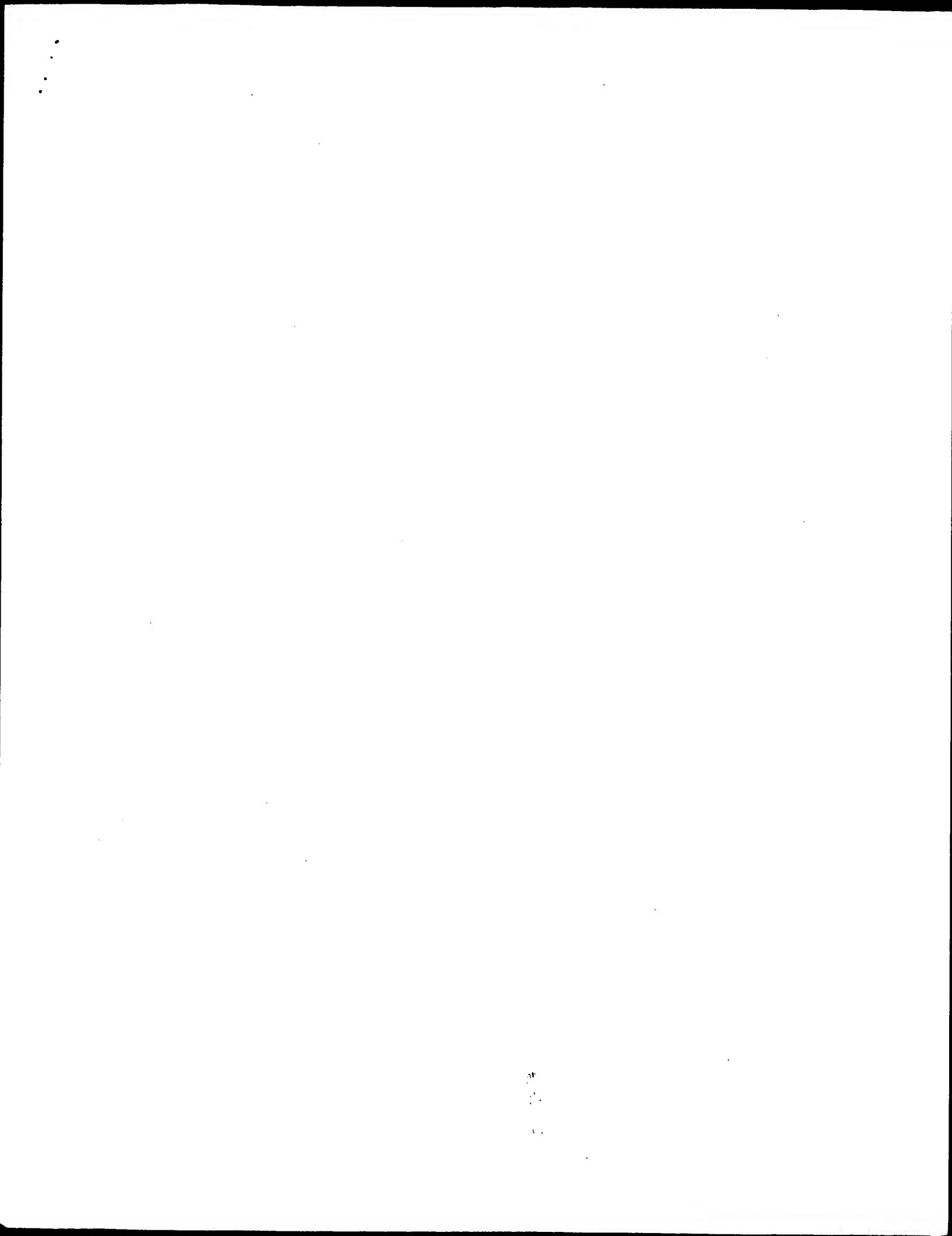
Wed Nov 13 14:22:41 2002

us-09-676-436-3.Limit.rni

Page 25

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	Matches 33; Conservative	0;	Mismatches 18;	Indels 0;	Gaps 0;
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Search completed: November 11, 2002, 10:47:56
Job time : 134 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 09:34:46 ; Search time 122 Seconds
(without alignments)
14511.307 Million cell updates/sec

Title: US-09-676-436-3
Perfect score: 4990
Sequence: 1 ctgaagactctccgatga.....ggtttatttaggaagctc 4990

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 100

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Maximum Match 100%
Listing first 1000 summaries

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- 2: /cgn2_6/ptodata/2/pubpna/PCIT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26.2	0.5	90	10	US-09-923-876-2711 Sequence 2711, Ap
2	25.8	0.5	81	10	US-09-864-761-31768 Sequence 772, A
3	25	0.5	91	10	US-09-864-761-31768 Sequence 31768, A
4	24.8	0.5	92	9	US-09-733-692A-31768 Sequence 31, App1
5	24.4	0.5	99	10	US-09-864-761-20908 Sequence 20908, A
6	24.2	0.5	80	10	US-09-864-761-28769 Sequence 28769, A
7	24.2	0.5	95	10	US-09-864-761-28328 Sequence 28328, A
8	24.2	0.5	99	10	US-09-864-761-25222 Sequence 25222, A
9	23.8	0.5	86	10	US-09-847-113-6 Sequence 6, App1
10	23.8	0.5	90	10	US-09-864-761-22288 Sequence 22288, A
11	23.6	0.5	100	10	US-09-969-373-453 Sequence 453, App
12	23.6	0.5	79	10	US-09-998-598-1313 Sequence 1313, App
13	23.6	0.5	92	10	US-09-783-590-9797 Sequence 9797, App
14	23.6	0.5	100	10	US-09-728-445-336 Sequence 336, App
15	23.4	0.5	70	10	US-09-923-876-1834 Sequence 1834, App
16	23.2	0.5	89	10	US-09-783-590-9597 Sequence 9597, App
17	23.2	0.5	93	10	US-09-864-761-20158 Sequence 20158, A
18	23.2	0.5	94	9	US-09-933-797-749 Sequence 749, App
19	23.2	0.5	96	10	US-09-864-761-27858 Sequence 27858, A

93	21	0.4	0.4	95	10	US-09-878-574-920	Sequence 920, App
94	21	0.4	0.4	96	10	US-09-864-761-22213	Sequence 22213, A
95	20.8	0.4	0.4	97	10	US-09-864-761-30639	Sequence 30639, A
96	20.8	0.4	0.4	98	10	US-09-974-300-4372	Sequence 4372, Ap
97	20.8	0.4	0.4	84	10	US-09-974-300-4391	Sequence 4391, Ap
98	20.8	0.4	0.4	85	10	US-09-974-300-4412	Sequence 4424, Ap
99	20.8	0.4	0.4	86	10	US-09-974-300-4412	Sequence 4412, Ap
100	20.8	0.4	0.4	87	10	US-09-974-300-4425	Sequence 4425, Ap
101	20.8	0.4	0.4	88	10	US-10-024-997-20	Sequence 20, Appl
102	20.8	0.4	0.4	89	10	US-09-864-761-26868	Sequence 26868, A
103	20.8	0.4	0.4	92	10	US-09-864-761-24698	Sequence 24698, A
104	20.8	0.4	0.4	94	10	US-09-864-761-21045	Sequence 21046, A
105	20.8	0.4	0.4	94	10	US-09-864-761-22895	Sequence 22895, A
106	20.8	0.4	0.4	95	10	US-09-969-373-656	Sequence 656, App
107	20.8	0.4	0.4	95	10	US-09-969-373-656	Sequence 656, App
108	20.8	0.4	0.4	99	10	US-09-864-761-28839	Sequence 28839, A
109	20.8	0.4	0.4	99	10	US-09-922-217-68	Sequence 68, Appl
110	20.8	0.4	0.4	99	10	US-09-833-263-68	Sequence 68, Appl
111	20.8	0.4	0.4	100	10	US-09-969-373-568	Sequence 508, App
112	20.6	0.4	0.4	70	10	US-09-466-320-18	Sequence 18, Appl
113	20.6	0.4	0.4	71	10	US-09-756-095-86	Sequence 86, Appl
114	20.6	0.4	0.4	77	8	US-08-978-633-30	Sequence 30, Appl
115	20.6	0.4	0.4	77	8	US-08-978-633-31	Sequence 31, Appl
116	20.6	0.4	0.4	77	8	US-08-978-634-31	Sequence 31, Appl
117	20.6	0.4	0.4	77	8	US-08-978-634-31	Sequence 31, Appl
118	20.6	0.4	0.4	77	8	US-08-978-637-30	Sequence 31, Appl
119	20.6	0.4	0.4	77	8	US-08-978-637-31	Sequence 31, Appl
120	20.6	0.4	0.4	77	8	US-08-978-632-30	Sequence 31, Appl
121	20.6	0.4	0.4	77	8	US-08-978-632-31	Sequence 31, Appl
122	20.6	0.4	0.4	78	9	US-09-766-700A-2	Sequence 2, Appli
123	20.6	0.4	0.4	80	10	US-09-923-876-370	Sequence 270, App
124	20.6	0.4	0.4	82	10	US-09-923-876-5283	Sequence 5283, App
125	20.6	0.4	0.4	82	10	US-09-864-761-26051	Sequence 26051, A
126	20.6	0.4	0.4	84	10	US-09-864-761-27108	Sequence 27108, A
127	20.6	0.4	0.4	87	10	US-09-864-761-23462	Sequence 23462, A
128	20.6	0.4	0.4	88	10	US-09-864-761-31450	Sequence 31450, A
129	20.6	0.4	0.4	90	8	US-08-837-459-24	Sequence 24, Appl
130	20.6	0.4	0.4	90	10	US-09-864-761-21971	Sequence 21971, A
131	20.6	0.4	0.4	92	10	US-09-969-373-514	Sequence 314, App
132	20.6	0.4	0.4	94	10	US-09-864-761-26559	Sequence 26559, A
133	20.6	0.4	0.4	96	9	US-09-864-441-261	Sequence 261, App
134	20.6	0.4	0.4	96	9	US-10-046-935-1699	Sequence 1699, App
135	20.6	0.4	0.4	97	9	US-09-878-574-14802	Sequence 14802, A
136	20.6	0.4	0.4	98	9	US-10-046-935-1575	Sequence 1575, App
137	20.6	0.4	0.4	98	9	US-09-923-217-992	Sequence 992, App
138	20.6	0.4	0.4	98	10	US-09-833-263-392	Sequence 392, App
139	20.6	0.4	0.4	98	10	US-09-969-373-115	Sequence 115, App
140	20.6	0.4	0.4	98	10	US-09-969-373-115	Sequence 115, App
141	20.6	0.4	0.4	98	10	US-09-864-761-23042	Sequence 23042, A
142	20.6	0.4	0.4	100	10	US-10-046-935-2169	Sequence 2169, App
143	20.4	0.4	0.4	57	9	US-09-783-590-836	Sequence 836, App
144	20.4	0.4	0.4	69	10	US-09-923-876-1834	Sequence 1834, App
145	20.4	0.4	0.4	70	10	US-09-960-352-8606	Sequence 8606, App
146	20.4	0.4	0.4	77	10	US-09-062-104A-11	Sequence 11, Appl
147	20.4	0.4	0.4	79	10	US-09-923-876-1489	Sequence 1489, App
148	20.4	0.4	0.4	82	10	US-09-923-876-1514	Sequence 1514, App
149	20.4	0.4	0.4	82	10	US-09-878-574-1572	Sequence 1572, App
150	20.4	0.4	0.4	89	10	US-09-864-761-30621	Sequence 30621, A
151	20.4	0.4	0.4	92	10	US-09-878-574-13556	Sequence 13556, A
152	20.4	0.4	0.4	93	10	US-09-759-143-220	Sequence 220, App
153	20.4	0.4	0.4	93	10	US-09-780-669-220	Sequence 220, App
154	20.4	0.4	0.4	93	10	US-09-030-606-220	Sequence 220, App
155	20.4	0.4	0.4	93	10	US-09-82-827-220	Sequence 220, App
156	20.4	0.4	0.4	93	10	US-09-115-453-220	Sequence 220, App
157	20.4	0.4	0.4	95	10	US-09-864-761-32571	Sequence 32571, A
158	20.4	0.4	0.4	96	10	US-09-864-761-22882	Sequence 22882, A
159	20.4	0.4	0.4	96	10	US-09-864-761-22882	Sequence 22882, A
160	20.4	0.4	0.4	97	10	US-09-864-761-30621	Sequence 30621, A
161	20.4	0.4	0.4	97	10	US-09-887-384A-112	Sequence 12, Appl
162	20.4	0.4	0.4	97	10	US-09-783-590-6702	Sequence 6702, App
163	20.4	0.4	0.4	98	10	US-09-969-373-779	Sequence 779, App
164	20.4	0.4	0.4	99	10	US-09-960-352-13299	Sequence 13299, A
165	20.4	0.4	0.4	100	10	US-09-864-761-17596	Sequence 17596, A

166	20.4	0.4	0.4	100	10	US-09-983-965-1122	Sequence 122, App
167	20.2	0.4	0.4	57	10	US-09-922-261-428	Sequence 428, App
168	20.2	0.4	0.4	67	10	US-09-923-501-759	Sequence 759, App
169	20.2	0.4	0.4	66	10	US-09-783-590-8768	Sequence 8768, App
170	20.2	0.4	0.4	69	10	US-09-922-217-929	Sequence 929, App
171	20.2	0.4	0.4	69	10	US-09-833-263-929	Sequence 929, App
172	20.2	0.4	0.4	69	10	US-09-983-965-3899	Sequence 3899, App
173	20.2	0.4	0.4	70	10	US-09-263-955-489	Sequence 489, App
174	20.2	0.4	0.4	72	10	US-09-923-876-3592	Sequence 3592, App
175	20.2	0.4	0.4	75	10	US-09-983-965-223	Sequence 223, App
176	20.2	0.4	0.4	78	10	US-09-864-761-26225	Sequence 26225, A
177	20.2	0.4	0.4	89	10	US-09-864-761-28181	Sequence 28181, A
178	20.2	0.4	0.4	89	10	US-09-864-761-29334	Sequence 29334, A
179	20.2	0.4	0.4	90	10	US-09-922-251-376	Sequence 376, App
180	20.2	0.4	0.4	91	10	US-09-878-574-5331	Sequence 5331, App
181	20.2	0.4	0.4	92	10	US-09-764-877-407	Sequence 407, App
182	20.2	0.4	0.4	93	10	US-09-864-761-17259	Sequence 17259, A
183	20.2	0.4	0.4	95	10	US-09-916-940-96	Sequence 96, Appl
184	20.2	0.4	0.4	95	10	US-09-916-940-96	Sequence 96, Appl
185	20.2	0.4	0.4	96	10	US-09-764-866-274	Sequence 274, App
186	20.2	0.4	0.4	97	10	US-09-923-876-14405	Sequence 14405, App
187	20.2	0.4	0.4	97	10	US-09-960-352-13934	Sequence 13934, A
188	20.2	0.4	0.4	98	10	US-09-960-352-13934	Sequence 13934, A
189	20.2	0.4	0.4	98	10	US-09-960-352-13934	Sequence 13934, A
190	20.2	0.4	0.4	99	10	US-09-864-761-29067	Sequence 29067, A
191	20.2	0.4	0.4	99	10	US-09-864-761-29354	Sequence 29354, A
192	20.2	0.4	0.4	99	10	US-09-960-352-699	Sequence 699, App
193	20.2	0.4	0.4	100	10	US-09-770-686-907	Sequence 907, App
194	20.2	0.4	0.4	100	10	US-09-924-035A-426	Sequence 426, App
195	20	0.4	0.4	51	10	US-09-976-787-25	Sequence 25, Appl
196	20	0.4	0.4	51	10	US-09-965-198-24	Sequence 24, Appl
197	20	0.4	0.4	56	10	US-09-967-013-81	Sequence 81, Appl
198	20	0.4	0.4	56	10	US-09-967-013-82	Sequence 82, Appl
199	20	0.4	0.4	59	10	US-09-967-013-82	Sequence 82, Appl
200	20	0.4	0.4	59	10	US-09-967-013-88	Sequence 88, Appl
201	20	0.4	0.4	59	10	US-09-967-013-88	Sequence 88, Appl
202	20	0.4	0.4	65	10	US-09-878-574-10483	Sequence 10483, A
203	20	0.4	0.4	67	12	US-09-920-300A-799	Sequence 799, App
204	20	0.4	0.4	69	10	US-10-033-528-799	Sequence 799, App
205	20	0.4	0.4	70	10	US-09-785-632-38	Sequence 38, Appl
206	20	0.4	0.4	73	10	US-09-983-965-417	Sequence 417, App
207	20	0.4	0.4	73	10	US-09-923-876-3060	Sequence 3060, App
208	20	0.4	0.4	77	10	US-09-864-761-29497	Sequence 29497, A
209	20	0.4	0.4	78	10	US-09-878-574-3746	Sequence 3746, App
210	20	0.4	0.4	80	10	US-09-764-877-445	Sequence 445, App
211	20	0.4	0.4	80	10	US-09-969-373-613	Sequence 613, App
212	20	0.4	0.4	83	10	US-09-284-0939-894	Sequence 894, App
213	20	0.4	0.4	87	10	US-09-864-761-17846	Sequence 17846, A
214	20	0.4	0.4	88	10	US-09-864-761-19737	Sequence 19737, A
215	20	0.4	0.4	88	10	US-09-864-761-31192	Sequence 31192, A
216	20	0.4	0.4	89	10	US-09-864-761-31259	Sequence 31259, A
217	20	0.4	0.4	89	10	US-09-783-590-2935	Sequence 2935, App
218	20	0.4	0.4	89	10	US-09-983-965-1255	Sequence 1255, App
219	20	0.4	0.4	90	10	US-09-815-242-3495	Sequence 3495, App
220	20	0.4	0.4	90	10	US-09-815-242-3495	Sequence 3495, App
221	20	0.4	0.4	90	10	US-09-815-242-3600	Sequence 3600, App
222	20	0.4	0.4	90	10	US-09-971-798-6	Sequence 6, Appl1
223	20	0.4	0.4	91	10	US-09-895-828-201	Sequence 201, App
224	20	0.4	0.4	92	10	US-09-864-761-27584	Sequence 27584, A
225	20	0.4	0.4	93	10	US-09-730-525-25	Sequence 25, Appl
226	20	0.4	0.4	93	10	US-09-730-525-25	Sequence 25, Appl
227	20	0.4	0.4	95	10	US-09-864-761-19747	Sequence 19747, A
228	20	0.4	0.4	95	10	US-09-864-761-28410	Sequence 28410, A
229	20	0.4	0.4	98	10	US-09-864-761-18752	Sequence 18752, A
230	20	0.4	0.4	98	10	US-09-864-761-21771	Sequence 21771, A
231	20	0.4	0.4	98	10	US-09-864-761-24060	Sequence 24060, A
232	20	0.4	0.4	98	10	US-09-864-761-30963	Sequence 30963, A
233	20	0.4	0.4	99	10	US-09-815-343-385	Sequence 385, App
234	20	0.4	0.4	100	10	US-09-864-761-19163	Sequence 19163, A
235	20	0.4	0.4	100	10	US-09-864-761-31630	Sequence 31630, A
236	20	0.4	0.4	100	10	US-09-864-761-32458	Sequence 32458, A
237	20	0.4					

239	19.8	0.4	63	10	US-09-811-672-4	Sequence 4, Appl 1	312	19.6	0.4	96	10	US-09-864-761-33016	Sequence 33016, A
240	19.8	0.4	63	10	US-09-983-965-2679	Sequence 2679, Ap	313	19.6	0.4	96	10	US-09-783-590-2031	Sequence 2031, A
241	19.8	0.4	66	10	US-09-896-888A-13	Sequence 13, Appl	314	19.6	0.4	96	10	US-09-912-679-32	Sequence 32, Appl
242	19.8	0.4	75	10	US-09-758-140-3	Sequence 9, Appl 1	315	19.6	0.4	98	10	US-09-864-761-13650	Sequence 13650, A
243	19.8	0.4	75	10	US-09-972-599A-9	Sequence 9, Appl 1	316	19.6	0.4	98	10	US-09-864-761-30912	Sequence 30912, A
244	19.8	0.4	75	10	US-09-972-599A-33	Sequence 33, Appl 1	317	19.6	0.4	100	10	US-09-969-373-1195	Sequence 1195, A
245	19.8	0.4	75	10	US-09-820-339A-3	Sequence 3, Appl 1	318	19.6	0.4	45	10	US-09-827-289-11	Sequence 11, Appl 1
246	19.8	0.4	76	10	US-09-864-761-26408	Sequence 26408, A	319	19.4	0.4	61	10	US-09-795-668-1342	Sequence 1342, Ap
247	19.8	0.4	76	10	US-09-864-761-31800	Sequence 31800, A	320	19.4	0.4	61	10	US-09-795-668-1342	Sequence 1342, Ap
248	19.8	0.4	77	10	US-09-864-761-22941	Sequence 22941, A	321	19.4	0.4	62	10	US-09-912-679-31	Sequence 31, Appl 1
249	19.8	0.4	77	10	US-09-878-574-10313	Sequence 10313, A	322	19.4	0.4	62	10	US-09-795-668-1303	Sequence 1303, Ap
250	19.8	0.4	79	10	US-09-919-580-499	Sequence 499, App	323	19.4	0.4	63	10	US-09-983-965-5121	Sequence 5121, Ap
251	19.8	0.4	80	10	US-09-827-289-7	Sequence 7, Appl 1	324	19.4	0.4	68	10	US-09-923-246-79	Sequence 79, Appl 1
252	19.8	0.4	80	10	US-09-827-289-8	Sequence 8, Appl 1	325	19.4	0.4	71	10	US-09-823-250-31	Sequence 31, Appl 1
253	19.8	0.4	81	10	US-09-864-761-26536	Sequence 26536, A	326	19.4	0.4	73	10	US-09-263-959-724	Sequence 724, App
254	19.8	0.4	82	10	US-09-864-761-33039	Sequence 33039, A	327	19.4	0.4	75	10	US-09-864-761-27031	Sequence 27031, A
255	19.8	0.4	84	10	US-09-864-761-18641	Sequence 18641, A	328	19.4	0.4	78	10	US-09-922-261-378	Sequence 378, App
256	19.8	0.4	87	10	US-09-864-761-25749	Sequence 25749, A	329	19.4	0.4	80	10	US-09-864-761-25594	Sequence 25594, A
257	19.8	0.4	87	10	US-09-864-761-31365	Sequence 31365, A	330	19.4	0.4	80	10	US-09-864-761-28951	Sequence 28951, A
258	19.8	0.4	87	10	US-09-969-373-837	Sequence 837, App	331	19.4	0.4	81	10	US-09-864-761-22617	Sequence 22617, A
259	19.8	0.4	88	10	US-09-864-761-24761	Sequence 24761, A	332	19.4	0.4	82	10	US-09-969-373-1056	Sequence 1056, Ap
260	19.8	0.4	89	10	US-09-983-965-4255	Sequence 4255, Ap	333	19.4	0.4	82	10	US-09-772-719-17	Sequence 37, Appl
261	19.8	0.4	90	10	US-09-864-761-26294	Sequence 26294, A	334	19.4	0.4	84	10	US-09-878-574-8869	Sequence 8869, Ap
262	19.8	0.4	90	10	US-09-864-761-27224	Sequence 27224, A	335	19.4	0.4	85	10	US-09-864-761-18967	Sequence 18967, A
263	19.8	0.4	90	10	US-09-972-599A-31	Sequence 31, Appl 1	336	19.4	0.4	87	10	US-09-864-761-22909	Sequence 22909, A
264	19.8	0.4	91	10	US-09-864-761-31491	Sequence 31491, A	337	19.4	0.4	87	10	US-09-864-761-27857	Sequence 27857, A
265	19.8	0.4	91	10	US-09-960-352-306	Sequence 306, Ap	338	19.4	0.4	87	10	US-10-024-997-88	Sequence 88, Appl
266	19.8	0.4	94	10	US-09-815-652-7	Sequence 7, Appl 1	339	19.4	0.4	87	12	US-09-864-761-29885	Sequence 2715, Ap
267	19.8	0.4	94	10	US-09-878-574-7191	Sequence 7191, Ap	340	19.4	0.4	88	10	US-09-983-965-2716	Sequence 2, Appl 1
268	19.8	0.4	95	10	US-09-960-352-3523	Sequence 3523, Ap	341	19.4	0.4	90	10	US-09-917-330-2	Sequence 17072, A
269	19.8	0.4	96	10	US-09-878-574-5248	Sequence 5248, Ap	342	19.4	0.4	91	10	US-09-864-761-17072	Sequence 17072, A
270	19.8	0.4	96	10	US-09-878-574-5248	Sequence 5248, Ap	343	19.4	0.4	92	10	US-09-864-761-18968	Sequence 18968, A
271	19.8	0.4	96	10	US-09-878-574-5248	Sequence 5248, Ap	344	19.4	0.4	92	10	US-09-864-761-18968	Sequence 18968, A
272	19.8	0.4	96	10	US-09-969-373-551	Sequence 551, App	345	19.4	0.4	93	10	US-09-969-373-1719	Sequence 1719, App
273	19.8	0.4	98	10	US-09-777-564-865	Sequence 865, App	346	19.4	0.4	95	10	US-09-864-761-32571	Sequence 32571, A
274	19.8	0.4	98	10	US-09-864-761-24557	Sequence 24557, A	347	19.4	0.4	95	10	US-09-960-352-8975	Sequence 8975, Ap
275	19.8	0.4	98	10	US-09-783-590-9853	Sequence 9853, Ap	348	19.4	0.4	96	10	US-09-864-761-151364	Sequence 151, App
276	19.8	0.4	99	10	US-09-864-761-30805	Sequence 30805, A	349	19.4	0.4	96	10	US-09-969-373-431	Sequence 431, App
277	19.8	0.4	99	10	US-09-864-761-30045	Sequence 30045, A	350	19.4	0.4	99	10	US-09-864-761-24821	Sequence 24821, A
278	19.8	0.4	99	10	US-09-815-242-1049	Sequence 1049, Ap	351	19.4	0.4	99	10	US-09-969-373-431	Sequence 431, App
279	19.8	0.4	100	10	US-09-783-590-10893	Sequence 10893, A	352	19.4	0.4	99	10	US-09-969-373-431	Sequence 431, App
280	19.8	0.4	100	10	US-09-867-701-2268	Sequence 2268, Ap	353	19.2	0.4	69	10	US-09-783-590-8150	Sequence 8150, Ap
281	19.6	0.4	50	9	US-09-992-598-45	Sequence 45, Appl	354	19.2	0.4	72	10	US-09-927-850-27	Sequence 27, Appl
282	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	355	19.2	0.4	75	10	US-09-864-761-26979	Sequence 26979, A
283	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	356	19.2	0.4	75	10	US-09-864-761-26979	Sequence 26979, A
284	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	357	19.2	0.4	77	10	US-09-922-217-374	Sequence 2406, A
285	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	358	19.2	0.4	78	10	US-09-922-217-374	Sequence 324, App
286	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	359	19.2	0.4	78	10	US-09-922-217-374	Sequence 2883, A
287	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	360	19.2	0.4	79	10	US-09-864-761-25883	Sequence 2883, A
288	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	361	19.2	0.4	83	10	US-09-864-761-25883	Sequence 2883, A
289	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	362	19.2	0.4	83	10	US-09-864-761-25883	Sequence 2883, A
290	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	363	19.2	0.4	84	10	US-09-864-761-25883	Sequence 2883, A
291	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	364	19.2	0.4	85	10	US-09-864-761-25883	Sequence 2883, A
292	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	365	19.2	0.4	85	10	US-09-864-761-25883	Sequence 2883, A
293	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	366	19.2	0.4	86	10	US-09-864-761-25883	Sequence 2883, A
294	19.6	0.4	56	10	US-09-738-363-25	Sequence 25, Appl	367	19.2	0.4	86	12	US-09-965-059-18	Sequence 82, Appl
295	19.6	0.4	67	10	US-09-815-242-1629	Sequence 1629, Ap	368	19.2	0.4	87	10	US-09-864-761-31392	Sequence 31392, A
296	19.6	0.4	68	10	US-09-909-652-6	Sequence 6, Appl 1	369	19.2	0.4	87	10	US-09-864-761-31392	Sequence 31392, A
297	19.6	0.4	81	10	US-09-864-761-32637	Sequence 32637, A	370	19.2	0.4	88	10	US-09-878-574-13597	Sequence 6199, Ap
298	19.6	0.4	81	10	US-09-864-761-32637	Sequence 32637, A	371	19.2	0.4	88	10	US-09-878-574-13597	Sequence 6199, Ap
299	19.6	0.4	82	10	US-09-783-590-1863	Sequence 1863, A	372	19.2	0.4	88	10	US-09-878-574-13597	Sequence 6199, Ap
300	19.6	0.4	85	10	US-09-864-761-20574	Sequence 20574, A	373	19.2	0.4	88	10	US-09-878-574-13597	Sequence 6199, Ap
301	19.6	0.4	85	10	US-09-864-761-22337	Sequence 22337, A	374	19.2	0.4	88	10	US-09-878-574-13597	Sequence 6199, Ap
302	19.6	0.4	86	10	US-09-864-761-22337	Sequence 22337, A	375	19.2	0.4	91	10	US-09-864-761-31101	Sequence 31101, A
303	19.6	0.4	86	10	US-09-864-761-22337	Sequence 22337, A	376	19.2	0.4	91	10	US-09-864-761-31101	Sequence 31101, A
304	19.6	0.4	87	9	US-09-933-797-135	Sequence 135, App	377	19.2	0.4	92	12	US-10-051-852-18	Sequence 18, Appl
305	19.6	0.4	88	10	US-09-864-761-18623	Sequence 18623, A	378	19.2	0.4	92	12	US-10-051-852-18	Sequence 18, Appl
306	19.6	0.4	88	10	US-09-864-761-21403	Sequence 21403, A	379	19.2	0.4	93	10	US-09-878-574-13845	Sequence 1894, Ap
307	19.6	0.4	89	10	US-09-969-373-346	Sequence 346, App	380	19.2	0.4	93	10	US-09-878-574-13845	Sequence 1894, Ap
308	19.6	0.4	92	10	US-09-864-761-27643	Sequence 27643, A	381	19.2	0.4	95	10	US-09-864-761-18159	Sequence 11865, Ap
309	19.6	0.4	94	10	US-09-864-761-24209	Sequence 24209, A	382	19.2	0.4	96	10	US-09-864-761-18159	Sequence 18159, A
310	19.6	0.4	96	9	US-10-046-935-1699	Sequence 1699, Ap	383	19.2	0.4	96	10	US-09-864-761-24349	Sequence 24349, A
311	19.6	0.4	96	10	US-09-864-761-30492	Sequence 30492, A	384	19.2	0.4	96	10	US-09-864-761-29751	Sequence 29751, A

C 385	19.2	0.4	97	10	US-09-969-373-960	Sequence 950, App	458	19	0.4	96	10	US-09-864-761-25639	Sequence 25639, A
C 387	19.2	0.4	98	10	US-09-864-761-26598	Sequence 26598, A	459	19	0.4	97	10	US-09-294-0938-840	Sequence 840, App
C 388	19.2	0.4	99	10	US-09-864-761-30787	Sequence 30787, A	C 460	19	0.4	97	10	US-09-864-761-27662	Sequence 27662, A
C 389	19.2	0.4	100	10	US-09-867-701-5615	Sequence 5615, Ap	C 461	19	0.4	98	10	US-09-783-590-9853	Sequence 9853, Ap
C 390	19.2	0.4	100	10	US-09-864-761-28542	Sequence 28542, A	C 462	19	0.4	99	10	US-09-864-761-12475	Sequence 12475, A
C 391	19.2	0.4	100	10	US-09-783-590-6064	Sequence 6064, Ap	C 463	19	0.4	99	12	US-10-033-558-1823	Sequence 1823, Ap
C 392	19.2	0.4	100	10	US-09-969-672-15	Sequence 15, Appl	C 464	19	0.4	100	10	US-09-864-761-18879	Sequence 18879, A
C 393	19.2	0.4	100	10	US-09-969-373-30	Sequence 30, Appl	C 465	19	0.4	100	10	US-09-864-761-24828	Sequence 24828, A
C 394	19.2	0.4	100	10	US-09-983-965-296	Sequence 296, App	C 466	19	0.4	100	10	US-09-864-761-231003	Sequence 31003, A
C 395	19.2	0.4	100	12	US-09-924-035A-289	Sequence 289, App	C 467	19	0.4	100	10	US-09-828-574-6085	Sequence 6085, Ap
C 396	19.2	0.4	47	10	US-09-765-527-244	Sequence 15, Appl	C 468	18.8	0.4	32	10	US-09-828-303-41	Sequence 41, Appl
C 397	19	0.4	49	10	US-09-179-536B-197	Sequence 244, App	C 469	18.8	0.4	37	10	US-09-882-303-58	Sequence 58, Appl
C 398	19	0.4	50	10	US-09-179-536B-198	Sequence 197, App	C 470	18.8	0.4	32	10	US-09-882-303-7	Sequence 7, Appl1
C 399	19	0.4	51	10	US-09-179-536B-199	Sequence 198, App	C 471	18.8	0.4	45	12	US-09-756-995-71	Sequence 13, Appl
C 400	19	0.4	52	10	US-09-179-536B-200	Sequence 199, App	C 472	18.8	0.4	47	10	US-09-147-142-23	Sequence 23, Appl
C 401	19	0.4	53	10	US-09-179-536B-201	Sequence 200, App	C 473	18.8	0.4	54	10	US-09-147-142-26	Sequence 26, Appl
C 402	19	0.4	54	10	US-09-179-536B-202	Sequence 201, App	C 474	18.8	0.4	60	10	US-09-294-0938-5594	Sequence 5594, Ap
C 403	19	0.4	54	10	US-09-922-261-325	Sequence 202, App	C 475	18.8	0.4	64	10	US-09-844-864-14	Sequence 14, Appl
C 404	19	0.4	55	10	US-09-179-536B-203	Sequence 203, App	C 476	18.8	0.4	65	12	US-10-021-758-15	Sequence 15, Appl
C 405	19	0.4	56	10	US-09-179-536B-204	Sequence 204, App	C 477	18.8	0.4	66	10	US-09-783-590-9281	Sequence 9281, Ap
C 406	19	0.4	57	10	US-09-848-164-49	Sequence 205, Appl	C 478	18.8	0.4	67	10	US-09-887-384-10	Sequence 10, Appl
C 407	19	0.4	57	10	US-09-179-536B-205	Sequence 206, App	C 479	18.8	0.4	67	10	US-09-815-242-1629	Sequence 1629, Ap
C 408	19	0.4	58	10	US-09-179-536B-206	Sequence 207, App	C 480	18.8	0.4	69	10	US-09-851-190A-12	Sequence 12, Appl
C 409	19	0.4	59	10	US-09-179-536B-207	Sequence 208, App	C 481	18.8	0.4	69	10	US-09-851-190A-12	Sequence 12, Appl
C 410	19	0.4	60	10	US-09-179-536B-208	Sequence 209, App	C 482	18.8	0.4	71	10	US-09-878-574-13067	Sequence 13067, A
C 411	19	0.4	61	10	US-09-179-536B-209	Sequence 210, App	C 483	18.8	0.4	72	9	US-09-832-659-22	Sequence 22, Appl
C 412	19	0.4	62	10	US-09-179-536B-210	Sequence 1, Appl1	C 484	18.8	0.4	72	10	US-09-812-679-29	Sequence 29, Appl
C 413	19	0.4	62	10	US-09-955-037-1	Sequence 11, App	C 485	18.8	0.4	74	10	US-09-294-0938-3534	Sequence 3534, Ap
C 414	19	0.4	63	10	US-09-179-536B-211	Sequence 211, App	C 486	18.8	0.4	75	10	US-09-960-352-6176	Sequence 6176, Ap
C 415	19	0.4	64	10	US-09-179-536B-212	Sequence 212, App	C 487	18.8	0.4	76	10	US-09-923-876-1833	Sequence 1833, Ap
C 416	19	0.4	65	10	US-09-179-536B-213	Sequence 213, App	C 488	18.8	0.4	77	10	US-09-864-761-33023	Sequence 33023, A
C 417	19	0.4	66	10	US-09-179-536B-214	Sequence 214, App	C 489	18.8	0.4	80	10	US-09-157-748-43	Sequence 43, Appl
C 418	19	0.4	67	10	US-09-179-536B-215	Sequence 215, App	C 490	18.8	0.4	80	10	US-09-864-761-23803	Sequence 23803, A
C 419	19	0.4	68	10	US-09-179-536B-216	Sequence 216, App	C 491	18.8	0.4	80	10	US-09-864-761-27154	Sequence 27154, A
C 420	19	0.4	69	10	US-09-179-536B-217	Sequence 217, App	C 492	18.8	0.4	80	10	US-09-764-846-267	Sequence 267, App
C 421	19	0.4	70	10	US-09-179-536B-218	Sequence 218, App	C 493	18.8	0.4	80	10	US-09-901-106-25	Sequence 25, Appl
C 422	19	0.4	71	10	US-09-179-536B-219	Sequence 219, App	C 494	18.8	0.4	80	10	US-09-925-301-764	Sequence 764, Ap
C 423	19	0.4	72	10	US-09-888-260-56	Sequence 220, App	C 495	18.8	0.4	81	9	US-09-864-761-33505	Sequence 33505, A
C 424	19	0.4	73	10	US-09-823-876-60	Sequence 221, App	C 496	18.8	0.4	82	10	US-09-878-574-3398	Sequence 3398, Ap
C 425	19	0.4	73	10	US-09-869-373-87	Sequence 60, Appl	C 497	18.8	0.4	83	10	US-09-294-0938-2319	Sequence 2319, Ap
C 426	19	0.4	73	10	US-09-983-965-5268	Sequence 87, Appl	C 498	18.8	0.4	85	10	US-09-781-804-55	Sequence 55, Appl
C 427	19	0.4	73	10	US-09-983-965-5268	Sequence 87, Appl	C 499	18.8	0.4	85	10	US-09-864-761-28595	Sequence 28595, A
C 428	19	0.4	75	10	US-09-758-140-7	Sequence 7, Appl1	C 500	18.8	0.4	86	10	US-09-960-352-11632	Sequence 11632, A
C 429	19	0.4	75	10	US-09-864-761-25911	Sequence 25911, A	C 501	18.8	0.4	87	10	US-09-864-761-33058	Sequence 33058, A
C 430	19	0.4	76	10	US-09-972-599A-7	Sequence 7, Appl1	C 502	18.8	0.4	87	10	US-09-764-877-3775	Sequence 3775, App
C 431	19	0.4	76	10	US-09-864-761-28047	Sequence 28047, A	C 503	18.8	0.4	88	10	US-09-815-343-279	Sequence 279, App
C 432	19	0.4	76	10	US-09-864-761-31463	Sequence 31463, A	C 504	18.8	0.4	88	10	US-09-764-869-1992	Sequence 1992, App
C 433	19	0.4	76	10	US-09-878-574-5227	Sequence 5227, Ap	C 505	18.8	0.4	88	10	US-09-334-923A-13	Sequence 13, Appl
C 434	19	0.4	77	10	US-09-783-590-3207	Sequence 3207, Ap	C 506	18.8	0.4	88	10	US-09-920-300A-1161	Sequence 1161, Ap
C 435	19	0.4	78	10	US-09-179-536B-25	Sequence 25, Appl	C 507	18.8	0.4	89	10	US-09-864-761-20966	Sequence 20966, A
C 436	19	0.4	78	10	US-09-864-761-23374	Sequence 23374, A	C 508	18.8	0.4	89	10	US-09-864-761-23401	Sequence 23401, A
C 437	19	0.4	79	9	US-09-733-692A-4	Sequence 4, Appl1	C 509	18.8	0.4	89	10	US-09-925-301-774	Sequence 774, App
C 438	19	0.4	79	10	US-09-864-761-20590	Sequence 20590, A	C 510	18.8	0.4	90	10	US-09-864-761-23699	Sequence 23699, A
C 439	19	0.4	80	10	US-09-864-761-31577	Sequence 31577, A	C 511	18.8	0.4	91	10	US-09-294-0938-1011	Sequence 1011, Ap
C 440	19	0.4	81	9	US-10-046-935-520	Sequence 520, App	C 512	18.8	0.4	91	10	US-09-864-761-21126	Sequence 21126, A
C 441	19	0.4	81	10	US-09-864-761-21838	Sequence 21838, A	C 513	18.8	0.4	91	10	US-09-864-761-25295	Sequence 25295, A
C 442	19	0.4	81	10	US-09-909-207-7	Sequence 7, Appl1	C 514	18.8	0.4	91	10	US-09-864-761-25331	Sequence 25331, Ap
C 443	19	0.4	81	10	US-09-909-207-8	Sequence 8, Appl1	C 515	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 444	19	0.4	81	10	US-09-949-559-115	Sequence 115, Appl	C 516	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 445	19	0.4	85	10	US-09-864-761-23322	Sequence 23322, A	C 517	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 446	19	0.4	85	10	US-09-864-761-25948	Sequence 25948, A	C 518	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 447	19	0.4	87	10	US-09-864-761-21228	Sequence 21228, A	C 519	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 448	19	0.4	88	10	US-09-864-761-30180	Sequence 30180, A	C 520	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 449	19	0.4	89	10	US-09-864-761-32525	Sequence 32525, A	C 521	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 450	19	0.4	90	12	US-10-003-496-7	Sequence 7, Appl1	C 522	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 451	19	0.4	91	10	US-09-864-761-24801	Sequence 24801, A	C 523	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 452	19	0.4	91	10	US-09-864-761-30056	Sequence 30056, A	C 524	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 453	19	0.4	92	10	US-09-923-876-4530	Sequence 4530, Ap	C 525	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 454	19	0.4	92	10	US-09-923-876-6277	Sequence 6277, Ap	C 526	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 455	19	0.4	92	10	US-09-864-761-30602	Sequence 30602, A	C 527	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 456	19	0.4	93	10	US-09-969-373-42	Sequence 42, Appl	C 528	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl
C 457	19	0.4	95	10	US-09-864-761-21583	Sequence 21583, A	C 529	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, Appl

531	18.8	0.4	92	10	US-09-864-761-25024	Sequence 25024, A	604	18.6	0.4	81	10	US-09-864-761-18720	Sequence 18720, A
532	18.8	0.4	92	12	US-10-029-913-3	Sequence 3, Appl1	605	18.6	0.4	81	10	US-09-864-761-20281	Sequence 26281, A
533	18.8	0.4	93	10	US-09-878-574-15698	Sequence 15698, A	606	18.6	0.4	81	10	US-09-815-242-566	Sequence 566, App
534	18.8	0.4	93	10	US-09-960-352-4510	Sequence 4510, Ap	607	18.6	0.4	81	10	US-09-922-661-251	Sequence 251, App
535	18.8	0.4	93	10	US-09-960-352-13791	Sequence 13791, A	608	18.6	0.4	82	10	US-09-777-564-1655	Sequence 1655, Ap
536	18.8	0.4	94	10	US-09-864-761-33109	Sequence 33109, A	609	18.6	0.4	82	10	US-09-864-761-20295	Sequence 20295, A
537	18.8	0.4	95	9	US-09-933-797-626	Sequence 626, App	610	18.6	0.4	84	9	US-10-060-841-8	Sequence 8, Appl1
538	18.8	0.4	95	10	US-09-864-761-31953	Sequence 31953, A	611	18.6	0.4	84	10	US-09-864-761-24579	Sequence 24579, A
539	18.8	0.4	95	10	US-09-878-574-299	Sequence 993, App	612	18.6	0.4	84	10	US-09-864-761-28712	Sequence 28712, A
540	18.8	0.4	95	10	US-09-919-580-246	Sequence 246, App	613	18.6	0.4	85	10	US-09-864-761-29373	Sequence 29376, A
541	18.8	0.4	95	10	US-09-969-373-1530	Sequence 1530, Ap	614	18.6	0.4	85	10	US-09-960-352-1628	Sequence 1628, Ap
542	18.8	0.4	96	10	US-09-864-761-20356	Sequence 20356, A	615	18.6	0.4	86	10	US-09-864-761-30207	Sequence 30207, A
543	18.8	0.4	96	10	US-09-864-761-26318	Sequence 26318, A	616	18.6	0.4	87	10	US-09-864-761-1904	Sequence 1904, Ap
544	18.8	0.4	96	10	US-09-864-761-23003	Sequence 23003, A	617	18.6	0.4	87	10	US-09-783-590-6677	Sequence 6677, Ap
545	18.8	0.4	96	10	US-09-963-965-2407	Sequence 2407, Ap	618	18.6	0.4	88	10	US-09-864-761-33186	Sequence 33186, A
546	18.8	0.4	97	10	US-09-938-938-5580	Sequence 5580, Ap	619	18.6	0.4	88	12	US-10-024-997-96	Sequence 96, Appl
547	18.8	0.4	97	10	US-09-864-761-22933	Sequence 22933, A	620	18.6	0.4	89	10	US-09-864-761-19599	Sequence 19599, A
548	18.8	0.4	97	10	US-09-864-761-22933	Sequence 22933, A	621	18.6	0.4	90	9	US-09-440-829-22	Sequence 22, Appl
549	18.8	0.4	97	10	US-09-815-242-306	Sequence 306, App	622	18.6	0.4	90	10	US-09-864-761-23367	Sequence 23367, A
550	18.8	0.4	97	10	US-09-969-373-532	Sequence 532, App	623	18.6	0.4	90	10	US-09-927-5994-25	Sequence 25, Appl
551	18.8	0.4	98	10	US-09-864-761-21839	Sequence 21839, A	624	18.6	0.4	90	10	US-09-878-574-5130	Sequence 5130, Ap
552	18.8	0.4	98	10	US-09-864-761-24634	Sequence 24634, A	625	18.6	0.4	91	10	US-09-864-761-17805	Sequence 17805, A
553	18.8	0.4	98	10	US-09-878-574-3830	Sequence 3830, Ap	626	18.6	0.4	91	10	US-09-864-761-18674	Sequence 18674, A
554	18.8	0.4	98	10	US-09-878-574-15211	Sequence 15211, A	627	18.6	0.4	91	10	US-09-864-761-22561	Sequence 22561, A
555	18.8	0.4	98	10	US-09-864-761-17733	Sequence 17733, A	628	18.6	0.4	91	10	US-09-815-242-1782	Sequence 1782, Ap
556	18.8	0.4	99	10	US-09-815-242-2244	Sequence 2244, Ap	629	18.6	0.4	91	10	US-09-815-242-1782	Sequence 1786, Ap
557	18.8	0.4	99	10	US-09-815-242-2244	Sequence 2244, Ap	630	18.6	0.4	91	10	US-09-783-590-11400	Sequence 11400, A
558	18.8	0.4	99	10	US-09-815-242-2244	Sequence 2244, Ap	631	18.6	0.4	91	10	US-09-969-373-2032	Sequence 2032, Ap
559	18.8	0.4	99	12	US-10-098-035-5	Sequence 5, Appl1	632	18.6	0.4	92	10	US-09-923-876-5032	Sequence 5032, Ap
560	18.8	0.4	100	10	US-09-770-696-06	Sequence 906, App	633	18.6	0.4	92	10	US-09-838-386-24	Sequence 31063, A
561	18.8	0.4	100	10	US-09-864-761-28443	Sequence 28443, A	634	18.6	0.4	93	10	US-09-864-761-28408	Sequence 28408, A
562	18.8	0.4	100	10	US-09-728-446-106	Sequence 106, App	635	18.6	0.4	94	10	US-09-755-830-10	Sequence 11100, A
563	18.8	0.4	100	10	US-09-919-580-428	Sequence 428, App	636	18.6	0.4	94	10	US-09-864-761-22634	Sequence 22634, A
564	18.8	0.4	100	10	US-09-908-855-57	Sequence 57, Appl	637	18.6	0.4	95	10	US-09-864-761-22634	Sequence 22632, A
565	18.8	0.4	100	10	US-09-867-701-9381	Sequence 9381, Ap	638	18.6	0.4	95	10	US-09-864-761-22634	Sequence 22632, A
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ALIGNMENTS

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RESULT 1
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; Sequence 2711, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Itc)
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Query Match
Best Local Similarity 56.3%; Score 26.2; DB 10; Length 90;
Matches 49; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

```

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QY 3570 GAGTACCGCAATGAGGAAGAAATATCATGCTGATGTTGATACGCTTACGTC 3629
Db 1 GACATACCTCGATGATGTTGAGCCAGGATTTCAATGAGAGGATTTGCTGCGCTTATGTC 60
QY 3630 CTATGATTAATGTTATGACGTTGGCTT 3656

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Db 61 ATTCGAGGCTGTTCTGACATTTGCTT 87

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RESULT 2
US-09-919-580-772/c
; Sequence 772, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; PRIOR APPLICATION NUMBER: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 772
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3, 4
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-772

```

```

Query Match
Best Local Similarity 57.0%; Score 25.8; DB 10; Length 81;
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

```

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QY 3723 CACCTCATCAGCGTCGACACCGGGAGCTGATGCCATGAAGAGATTCATTCAACC 3782
Db 79 CAGCAGCAAGCAGGTCATCCTTTGGGGAGCAGAGCCCAATMAAGTTCAGACTCAAAA 20
QY 3783 TAATGACATTAAGCTATC 3801
Db 19 AAAAAAAAAAAGGCGCNC 1

```

```

RESULT 3
US-09-864-761-31768/c
; Sequence 31768, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aemica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR APPLICATION NUMBER: 2001-05-23
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669

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```

: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 31768
: LENGTH: 91
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC007684.2
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
: OTHER INFORMATION: EST HUMAN HIT: A1273296.1, EVALUATE 3.00e-44
: OTHER INFORMATION: NT HIT: G14506376, EVALUATE 2.00e-44
: OTHER INFORMATION: SWISSPROT HIT: P41892, EVALUATE 2.40e-02
: US-09-664-761-31768
:
: Query Match
: Best Local Similarity 61.5%; Score 25; DB 10; Length 91;
: Matches 40; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
:
: QY 3815 ACGAATGAAATATTCGAGCGATCAACACCCCATCGGTGCTTTGGTGG 3874
: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: DB 67 AAGAATATATATGATGAAAGACGTGAACACCCCAATATGCTTATTTGAAGCT 8
: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: QY 3875 AGCTC 3879
: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: DB 7 ATCTC 3
:
: RESULT 4
: US-09-733-692A-31/C
: Sequence 31, Application US/09733692A
: GENERAL INFORMATION:
: APPLICANT: Murphy, Brian R.
: APPLICANT: Collins, Peter L.
: APPLICANT: Schmidt, Alexander C.
: APPLICANT: Durbin, Anna P.
: APPLICANT: Skidopoulos, Mario H.
: APPLICANT: Tao, Tao
: TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIVS) AS
: TITLE OF INVENTION: VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
: FILE OF INVENTION: BY PIV AND OTHER HUMAN PATHOGENS
: FILE REFERENCE: 15280-40410US
: CURRENT APPLICATION NUMBER: US/09/733,692A
: PRIOR FILING DATE: 2000-12-08
: PRIOR APPLICATION NUMBER: 60/170,195
: PRIOR FILING DATE: 1999-12-10
: NUMBER OF SEQ ID NOS: 62
: SOFTWARE: Patent Ver. 2.1
: SEQ ID NO 31
: LENGTH: 92
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Reverse primer

```

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: OTHER INFORMATION: for RSV A G gene insert
: US-09-733-692A-31
:
: Query Match
: Best Local Similarity 63.3%; Score 24.8; DB 9; Length 92;
: Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
:
: QY 45 TACCTGCCCCCGACGACAGATGAAACGATGTCAACCAACATCAGAGAA 104
: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: DB 80 TTCATCTCCACCAACACACGACGACAGTAAAGTAAGAAAAAATTAGATTAA 21
:
: RESULT 5
: US-09-664-761-20908/C
: Sequence 20908, Application US/09664761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
: FILE REFERENCE: Aecm1ca-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: PRIOR FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 20908
: LENGTH: 99
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC009305.1
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.78
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.8

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OTHER INFORMATION: NT HIT: AJ271735.1, EVALUE 1.80e-01
OTHER INFORMATION: EST_HUMAN HIT: A1444613.1, EVALUE 8.50e-01
US-09-864-761-20908

Query Match
Best Local Similarity 0.5%; Score 24.4; DB 10; Length 99;
Matches 43; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 751 AATGATCTTCTAGAGAGCGAGTCCACCTCTTGAGCAACAAGATTGAGTTAC 810
DB 94 AATATGATGCGCTAGCATGGATCCAGCCCTGCGCAGACCAATGATGATCTCTC 35
QY 811 TCACACATCATCTCA 824
DB 34 TGACCTCATCATCA 21

RESULT 6
US-09-864-761-28769/c
Sequence 28769, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 28769
LENGTH: 80
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL121582.14
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.85
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.88
OTHER INFORMATION: EST_HUMAN HIT: BF475330.1, EVALUE 9.50e-01
US-09-864-761-28769

Query Match
Best Local Similarity 0.5%; Score 24.2; DB 10; Length 80;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 3462 AACAGAACTTGGAGCTTGGACACTAATTCAGCCAGAGTAAGATTACTGCTTAACCT 3521
DB 66 AAGAAATTTATCAGACACTGTGGACATTTAAAGCCACAGAAATATCTCTGTTAAATT 7
QY 3522 A 3522
DB 6 A 6

RESULT 7
US-09-864-761-28328/c
Sequence 28328, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30

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1 RESULT 8
2 US-09-864-761-25222
3 ; Sequence 25222, Application US/09864761
4 ; Patent No. US20020048763A1
5 GENERAL INFORMATION:
6 APPLICANT: Penn, Sharon G.
7 APPLICANT: Rank, David R.
8 APPLICANT: Hanzel, David K.
9 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
10 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
11 FILE REFERENCE: A06m1ca-X-1
12 CURRENT APPLICATION NUMBER: US/09/864,761
13 CURRENT FILING DATE: 2001-05-23
14 PRIOR APPLICATION NUMBER: US 60/180,312
15 PRIOR FILING DATE: 2000-02-04
16 PRIOR APPLICATION NUMBER: US 60/207,456
17 PRIOR FILING DATE: 2000-05-26
18 PRIOR APPLICATION NUMBER: US 09/632,366
19 PRIOR FILING DATE: 2000-08-03
20 PRIOR APPLICATION NUMBER: GB 24263.6
21 PRIOR FILING DATE: 2000-10-04
22 PRIOR APPLICATION NUMBER: US 60/236,359
23 PRIOR FILING DATE: 2000-09-27
24 PRIOR APPLICATION NUMBER: PCT/US01/00666
25 PRIOR FILING DATE: 2001-01-30
26 PRIOR APPLICATION NUMBER: PCT/US01/00667
27 PRIOR FILING DATE: 2001-01-30
28 PRIOR APPLICATION NUMBER: PCT/US01/00664
29 PRIOR FILING DATE: 2001-01-30
30 PRIOR APPLICATION NUMBER: PCT/US01/00669
31 PRIOR FILING DATE: 2001-01-30
32 PRIOR APPLICATION NUMBER: PCT/US01/00665
33 PRIOR FILING DATE: 2001-01-30
34 PRIOR APPLICATION NUMBER: PCT/US01/00668
35 PRIOR FILING DATE: 2001-01-30
36 PRIOR APPLICATION NUMBER: PCT/US01/00663
37 PRIOR FILING DATE: 2001-01-30
38 PRIOR APPLICATION NUMBER: PCT/US01/00662
39 PRIOR FILING DATE: 2001-01-30

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      RESULT 9
      US-09-847-113-6
      ; Sequence 6, Application US/09847113
      ; Patent No. US20020121314A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Yu, Changjun
      ; TITLE OF INVENTION: Target Analyte Detection Using Asymmetrical Self-Assembled Monolayers
      ; FILE REFERENCE: A-69306-1
      ; CURRENT APPLICATION NUMBER: US/09/847,113
      ; CURRENT FILING DATE: 2001-05-01
      ; PRIOR APPLICATION NUMBER: 60/201,026
      ; PRIOR FILING DATE: 2000-05-01
      ; PRIOR APPLICATION NUMBER: 09/626,096
      ; PRIOR FILING DATE: 2000-07-26
      ; NUMBER OF SEQ ID NOS: 9
      ; SOFTWARE: Patentin version 3.1
      ; SEQ ID NO 6
      ; LENGTH: 86
      ; TYPE: DNA
      ; ORGANISM: Artificial Sequence
      ; FEATURE:
      ; OTHER INFORMATION: sandwich assay target and signaling probe.
      US-09-847-113-6

      Query Match          0.5%;      Score 23.8;  DB 10;  Length 86;
      Best Local Similarity 59.7%;      Pred. No. 3.7e+03;
      Matches 40;  Conservative 0;  Mismatches 27;  Indels 0;  Gaps 0;

      QY      3871  GTGGAGCTTCATAGAGAAAGTATGTCATCTTCATGAGACTACTGGCATGAGGGAGCTTTA 3930
              |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      Db       5      GTGGGGGAGCATCAACAGCAGCCATGCAAAATGTATAAAGAGAGACCATCATCAAGAGAACTGCA 64
              |||  |||  |||

```


Db 1 1 1 1
8 AAAA 3

RESULT 13

US-09-783-590-9797
; Sequence 9797, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillion, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Steven M.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16, 2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: Patentlin Ver. 2.0
; SEQ ID NO 9797
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (31)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (32)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (53)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (65)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (81)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (83)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (92)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-9797

Query Match

Best Local Similarity 0.5%; Score 23.6; DB 10; Length 92;
55.4%; Pred. No. 4.5e+03;
Matches 41; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 498 AAAGCTTACCTGCTCAAGAAAAAGACAGGAGCAAGCAAGAAATACGTC 557

Db 4 AGAGGAAACCTGATTAATAAAGAAAAAGAAAGAAAGATGTAATATATATC 63

OY 558 TGGTTCTGGCTTA 571

Db 64 TNCCTTCTAGGCTA 77

RESULT 14

US-09-728-445-336
; Sequence 336, Application US/09728445
; Patent No. US20020102543A1
; GENERAL INFORMATION:
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. US20020102543A1el Mutated Mammalian Cells and

; FILE REFERENCE: LEX-0102-USA
; CURRENT APPLICATION NUMBER: US/09/728,445
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 336
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-728-445-336

Query Match

Best Local Similarity 0.5%; Score 23.6; DB 10; Length 100;
56.4%; Pred. No. 4.7e+03;
Matches 44; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

OY 3431 CATATCCAGAGAGATTCAGTTCACACAGAAAGTTGGACACTTGGACACTAA 3490

Db 17 CACGTCAGAGAGAAAGCCAGATGGCCAGAGAGAAAGTCACTGTTGAACATGTTGG 76

OY 3491 TCAGCCAGATTAAGATA 3508

Db 77 ACAGAGAGAGTCAAGAAA 94

RESULT 15

US-09-923-876-1834
; Sequence 1834, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Lalquidi, Raghnath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: Perl Program
; SEQ ID NO 1834
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700159608H2
; NAME/KEY: unsure
; LOCATION: 43, 50, 52-53, 61, 63, 67, 69
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-1834

Query Match

Best Local Similarity 0.5%; Score 23.4; DB 10; Length 70;
55.4%; Pred. No. 4.2e+03;
Matches 36; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

OY 486 ACAGCTTTGCTTAACCTTACTCTCAAGAAAAAGACAGGAGCAAGAGAGACA 545

Db 6 ACACCTTTGTATATATATCTACAGTTTGTGAGAAANANANANANANANANNA 65

OY 546 AGAA 550

Db 66 ANANA 70

RESULT 16

US-09-783-590-9597/c

```
Sequence 9597, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
PRIOR APPLICATION NUMBER: 2000-02-15
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9597
LENGTH: 89
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (59)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-9597
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```
Query Match 0.5%; Score 23.2; DB 10; Length 89;
Best Local Similarity 64.2%; Pred. No. 5.7e+03;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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QY 1967 AATATCTGTAGAGAAATGCAATTTACCAAGAAATACTGATTACATA 2019
DB 81 AGAATCTGCTGGAAAAAATMAAATAATAATAATAATAATAATAATA 29
```

```
RESULT 17
US-09-864-761-20158
Sequence 20158, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION NUMBER: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,386
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20158
LENGTH: 93
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL109615.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.2
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.6
OTHER INFORMATION: EST_HUMAN HIT: BE97335.1, EVALUATE 1.10e+00
OTHER INFORMATION: SWISSPROT HIT: 054828, EVALUATE 7.00e+00
OTHER INFORMATION: NT HIT: 294043.1, EVALUATE 7.70e-01
US-09-864-761-20158
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Query Match 0.5%; Score 23.2; DB 10; Length 93;
Best Local Similarity 61.7%; Pred. No. 5.8e+03;
Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
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QY 2496 CTATCTGCTTGCACAGCAGCGTGATCGAGCCCGTATTCAGAGCAGCGTGGGCAC 2555
DB 15 CTGCTGTTGGGGCCACAGCAGCAGGAGCGAGGATCTGCGATGAAGGGGCAC 74
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RESULT 18
US-09-933-797-749/C
Sequence 749, Application US/09933797
Patent No. US2002015119A1
GENERAL INFORMATION:
APPLICANT: Robert A. Sikes et al.
TITLE OF INVENTION: Isolation and Use of Fetal Urogenital
FILE REFERENCE: 9901-007-999
CURRENT APPLICATION NUMBER: US/09/933,797
PRIOR APPLICATION NUMBER: US/09/482,933
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: PCT/US99/10746
PRIOR FILING DATE: 1999-05/14
PRIOR APPLICATION NUMBER: 60/085,383
PRIOR FILING DATE: 1998-05-14
NUMBER OF SEQ ID NOS: 811
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 749
LENGTH: 94
TYPE: DNA
ORGANISM: Murine
US-09-933-797-749
Query Match 0.5%; Score 23.2; DB 9; Length 94;
Best Local Similarity 53.7%; Pred. No. 5.9e+03;
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OTHER INFORMATION: MAP TO AC005195.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.55
OTHER INFORMATION: SWISSPROT HIT: P17588, EVALUATE 2.50e+00
US-09-864-761-32598

Query Match
Best Local Similarity 0.58; Score 23.2; DB 10; Length 96;
Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 4457 TTGCGACAGATGAAGATGACCTAGTACATATGACTTGGAAATCTCTTATTCAC 4516
Db 63 TTGCGACAGATGAAGATGATGATGCTGCGCTGCGGCTGAGCTTCTCTCAATTCAC 4

RESULT 21
US-09-864-761-25187
Sequence 25187, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 25187
LENGTH: 97
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011449.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN HEEL, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
OTHER INFORMATION: EST_HUMAN HIT: BE393813.1, EVALUATE 9.00e-48
OTHER INFORMATION: NT HIT: M28624.1, EVALUATE 5.20e-02
US-09-864-761-25187

Query Match
Best Local Similarity 0.58; Score 23.2; DB 10; Length 97;
Matches 40; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 140 AAGAAATGAATGACCAATGACCTCCACATTAAGACACGTGAAGAAACAGTGGAGA 199
Db 1 ATGAACACCAATGAAGACACTAGTTAAACTTAAGGAAATGAGAAAGACAGAGAGA 60
QY 200 ATGTGGAA 207
Db 61 AAGCTCAA 68

RESULT 22
US-09-864-761-25976/C
Sequence 25976, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203

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? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
? SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
? SEQ ID NO 25976
? LENGTH: 84
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AP000347.1
? OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
? OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
? OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.3
? OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
? OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
? OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8
? OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.8
? OTHER INFORMATION: NT HIT: g111434115, EVALUE 9.00e-25
? OTHER INFORMATION: EST HUMAN HIT: BE771814.1, EVALUE 1.00e-37
? OTHER INFORMATION: SWISSPROT HIT: P04424, EVALUE 9.00e-07
? US-09-864-761-25976

Query Match
Best Local Similarity 57.7%; Score 23; DB 10; Length 84;
Matches 41; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Oy 1817 TGCAGAGGTTCTGGAGGACTTGGAGAGCCGACTGCAACATTGACGCTTTGAGAGG 1876
Db 83 TGCATATAGTGTTGAGGAGTGCCGCCACCTTCAACTCAACCCCAATGATGAGG 24
Oy 1877 ATCTACATATA 1887
Db 23 ACATCCACACA 13

RESULT 23
US-09-864-761-33084/C
? Sequence 33084, Application us/09864761
? Patent No. US20020048763A1
? GENERAL INFORMATION:
? APPLICANT: Penn, Sharon G.
? APPLICANT: Rank, David R.
? APPLICANT: Hanzel, David K.
? APPLICANT: Chen, Wensheng
? TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
? FILE REFERENCE: Aecm1ca-X-1
? CURRENT FILING DATE: 2001-05-23
? PRIOR APPLICATION NUMBER: US/09/864,761
? PRIOR FILING DATE: 2000-02-04
? PRIOR APPLICATION NUMBER: US 60/180,312
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: US 60/207,456
? PRIOR FILING DATE: 2000-08-03
? PRIOR APPLICATION NUMBER: US 09/632,366
? PRIOR FILING DATE: 2000-10-04
? PRIOR APPLICATION NUMBER: GB 24263,6
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: US 60/236,359
? PRIOR FILING DATE: 2000-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00666
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00667
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00664
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00669
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00665
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00668
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00663
? PRIOR FILING DATE: 2001-01-30
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? PRIOR APPLICATION NUMBER: PCT/US01/00662
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00661
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 09/608,408
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: US 09/774,203
? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
? SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
? SEQ ID NO 33084
? LENGTH: 84
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AC009401.1
? OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
? OTHER INFORMATION: EST HUMAN HIT: AM237754.1, EVALUE 3.00e-03
? OTHER INFORMATION: SWISSPROT HIT: O15360, EVALUE 5.40e+00
? OTHER INFORMATION: NT HIT: AF092030.2, EVALUE 4.30e-02
? US-09-864-761-33084

Query Match
Best Local Similarity 68.1%; Score 23; DB 10; Length 84;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 2919 CAATTGATTTGATGATATCATATAAGAGTTGTCGTTTGATGATCTG 2965
Db 73 CATTTTTCCTTTAGTACCTTAAGAGATGTCGCTGCTTCTTTTGG 27

RESULT 24
US-09-864-761-27237/C
? Sequence 27237, Application us/09864761
? Patent No. US20020048763A1
? GENERAL INFORMATION:
? APPLICANT: Penn, Sharon G.
? APPLICANT: Rank, David R.
? APPLICANT: Hanzel, David K.
? APPLICANT: Chen, Wensheng
? TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
? FILE REFERENCE: Aecm1ca-X-1
? CURRENT FILING DATE: 2001-05-23
? PRIOR APPLICATION NUMBER: US/09/864,761
? PRIOR FILING DATE: 2000-02-04
? PRIOR APPLICATION NUMBER: US 60/180,312
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: US 60/207,456
? PRIOR FILING DATE: 2000-08-03
? PRIOR APPLICATION NUMBER: US 09/632,366
? PRIOR FILING DATE: 2000-10-04
? PRIOR APPLICATION NUMBER: GB 24263,6
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: US 60/236,359
? PRIOR FILING DATE: 2000-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00666
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00667
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00664
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00669
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00665
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00668
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00663
? PRIOR FILING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/864,761
 PRIOR FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30

1 CURRENT APPLICATION NUMBER: US/09/864,761
 2 CURRENT FILING DATE: 2001-05-23
 3 PRIOR APPLICATION NUMBER: US 60/180,312
 4 PRIOR FILING DATE: 2000-02-04
 5 PRIOR APPLICATION NUMBER: US 60/207,456
 6 PRIOR FILING DATE: 2000-05-26
 7 PRIOR APPLICATION NUMBER: US 09/632,366
 8 PRIOR FILING DATE: 2000-08-03
 9 PRIOR APPLICATION NUMBER: GB 24263,6
 10 PRIOR FILING DATE: 2000-10-04
 11 PRIOR APPLICATION NUMBER: US 60/236,359
 12 PRIOR FILING DATE: 2000-09-27
 13 PRIOR APPLICATION NUMBER: PCT/US01/00666
 14 PRIOR FILING DATE: 2001-01-30
 15 PRIOR APPLICATION NUMBER: PCT/US01/00667
 16 PRIOR FILING DATE: 2001-01-30
 17 PRIOR APPLICATION NUMBER: PCT/US01/00664
 18 PRIOR FILING DATE: 2001-01-30

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PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 31482
LENGTH: 87
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007567.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: NT HIT: AL163303.2, EVALUATE 1.00e-05
OTHER INFORMATION: EST HUMAN HIT: BE221737.1, EVALUATE 1.00e-03
OTHER INFORMATION: SWISSPROT HIT: P13186, EVALUATE 1.10e+00
US-09-864-761-31482

Query Match
Best Local Similarity 62.1%; Pred. No. 7.3e+03; Length 87;
Matches 36; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Oy 3215 GTTTCACCTTGGCATGACGAGACGCCGCTGATGAGGACCTGATGACCA 3272
Db 60 GTTTCACCTTGGCATGACGAGACGCCGCTGATGAGGACCTGATGACCA 3

RESULT 27
US-09-864-761-32824/c
Sequence 32824, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30

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PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 32824
LENGTH: 89
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL030997.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.93
OTHER INFORMATION: NT HIT: M96655.1, EVALUATE 1.80e-01
US-09-864-761-32824

Query Match
Best Local Similarity 56.8%; Pred. No. 7.4e+03; Length 89;
Matches 42; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Oy 1981 GAGATGATGATTTCCACCAAGAAATATCATCTAGCGGAGAGACAGACAGGC 2040
Db 86 GAGATGATGATTTCCACCAAGAAATATCATCTAGCGGAGAGACAGACAGGC 27

Oy 2041 GCGAAGCTTTCTCG 2054
Db 26 CCGAAGCTTATCTG 13

RESULT 28
US-09-923-876-1300
Sequence 1300, Application US/09923876
Patent No. US20020013958A1
GENERAL INFORMATION:
APPLICANT: Lalquid, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PI-0012-1 CON
CURRENT FILING DATE: 2001-08-06
PRIORITY APPLICATION NUMBER: 09/298,329
PRIORITY FILING DATE: 1999-04-21
PRIORITY APPLICATION NUMBER: 60/085,331
PRIORITY FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 1300
LENGTH: 98
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc-feature

```

OTHER INFORMATION: Incycle ID No. US20020013958A1 700158456H1
NAME/KEY: unsure
LOCATION: 93
OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-1300

Query Match
Best Local Similarity 0.58; Score 22.8; DB 10; Length 98;
Matches 45; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 1102 TCCAAAGCTAATGAGCCGAGTATGAGGTGATGACACAGAGCAATTAAGGAGTTG 1161

DB 12 TACACAGTACTGCTGCTGGGCAATTGAGACCATGACAGAAAGTATTGGAGAGGCT 71

OY 1162 GAAAGTACTAGCAGATGAGAGTGA 1184

DB 72 AAAAGCTACACGACGAGAGAGCNA 94

RESULT 29

US-09-919-580-637/C
Sequence 637, Application US/09919580
Patent No. US20020110832A1

GENERAL INFORMATION:

APPLICANT: Pyle, Ruth

APPLICANT: Xu, Jiangchun

APPLICANT: Scientist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.552

CURRENT APPLICATION NUMBER: US/09/919,580

CURRENT FILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 934

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 637

LENGTH: 64

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: 56

OTHER INFORMATION: n = A,T,C or G

US-09-919-580-637

Query Match

Best Local Similarity 0.5%; Score 22.6; DB 10; Length 64;
Matches 37; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 498 AAAGCTTACCTGAGCTCAAGAAAAAGACGAGCAAGAGGACAAAGAAATACGTC 557

DB 64 AAGGCTTTTCTTTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGGCG 5

OY 558 TG 559

DB 4 GC 3

RESULT 30

US-09-878-574-7267/C

Sequence 7267, Application US/09878574
Patent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and other Molecules Associated with

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 7267
LENGTH: 96
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 70109674H1
US-09-878-574-7267

Query Match
Best Local Similarity 0.58; Score 22.6; DB 10; Length 96;
Matches 46; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

OY 4533 TACATTAAGACTGCTGACAGAGCATATAGGCTTTTAACCTCCAGACTGAAGACT 4592

DB 86 TACGTGATGCTGTGACAGACTGACAGAGAGTTGTCGACACTGCAGATTCAAATTAAT 27

OY 4593 GCACAGGTGACACAGCTTCTTC 4617

DB 26 GCAGAGGGGAAACGCTTACGCTTC 2

RESULT 31

US-09-864-761-24215

Sequence 24215, Application US/09864761
Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

SEQ ID NO 24215

```
LENGTH: 98
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL096863.10
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.87
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
OTHER INFORMATION: NT HIT: M36383.1, EVALUATE 3.206+00
US-09-864-761-24215

Query Match
Best Local Similarity 58.0%; Score 22.6; DB 10; Length 98;
Matches 40; Conservative 0; Pred. No. 9e+03; 29; Indels 0; Gaps 0;
Mismatches 29;

OY 956 TCCAGACAGGCTGCGACCTCTGTTGCTTAACATCACAAGACTTAATCAGA 1015
DB 7 TTCTGCACTATTGGAAGTACTATGTTGATTTGTAATAAATACAGAGTCTTCTCAT 66

OY 1016 AATTAGA 1024
DB 67 CACTACTGA 75

RESULT 32
US-09-864-761-25667
Sequence 25667, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Accmics-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
```

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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Snpmax Sequence Listing Engine vers. 1.1
SEQ ID NO: 25667
LENGTH: 100
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005300.10
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: NT HIT: 916678436, EVALUATE 2.10e-01
OTHER INFORMATION: EST HUMAN HIT: BE159343.1, EVALUATE 1.00e-49
OTHER INFORMATION: SWISSPROT HIT: P04468, EVALUATE 5.50e+00
US-09-864-761-25667

Query Match
Best Local Similarity 58.0%; Score 22.6; DB 10; Length 100;
Matches 40; Conservative 0; Pred. No. 9.2e+03; 29; Indels 0; Gaps 0;
Mismatches 29;

OY 3242 GCCCGCTGCTATGAGTACCTGATGCCATAGTACCTCTTAACCCACACCTCATTA 3301
DB 26 GCCCTCCACCTCTGCATGCTCTTCATGCCCATGCCCTCCAGATCCATGACCTGG 85

OY 3302 TCCCCACTC 3310
DB 86 TCCACACTC 94

RESULT 33
US-09-878-574-14838
Sequence 14838, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO: 14838
LENGTH: 83
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701069318H1
US-09-878-574-14838

Query Match
Best Local Similarity 59.4%; Score 22.4; DB 10; Length 83;
Matches 38; Conservative 0; Pred. No. 9.1e+03; 26; Indels 0; Gaps 0;
Mismatches 26;

OY 3177 TGGCATTGTCATAGGAACACACAGTCTGTTACAGGTTTGTACTTCCCATTCATCG 3236
DB 6 TGGTGTGTCGCGAGCAAAACCAAGCATCTACTTGTCTGTCACAGATGCTCT 65

OY 3237 GAAC 3240
DB 66 GATC 69
```


OTHER INFORMATION: SWISSPROT HIT: O43236, EVALUE 1.00e-12
OTHER INFORMATION: NT HIT: U08870.1, EVALUE 1.00e-49
OTHER INFORMATION: EST_HUMAN HIT: AN964640.1, EVALUE 1.00e-49
US-09-864-761-27593

Query Match 0.4%; Score 22.4; DB 10; Length 100;
Best Local Similarity 66.7%; Pred. No. 1e+04; 16; Indels 0; Gaps 0;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2566 CAGCCTGTCAAGTCCTCAGTGTGAGACCTGTGACACCTGAGA 2613
DB 60 CAGCGGTCACATCTGCTATCTGCTTAAGGACAGACACTGACA 13

RESULT 36
US-09-864-761-24218/c
Sequence 24218, Application US/09864761
GENERAL INFORMATION:
PATENT No. US20020048763A1
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 24218
LENGTH: 75
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: MAP TO AC013746.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.8
US-09-864-761-24218

Query Match 0.4%; Score 22.2; DB 10; Length 75;
Best Local Similarity 69.8%; Pred. No. 9.7e+03;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 193 GTGAGATGTGCAACATATACCTTAAGCAGCAGAAAGA 235
DB 73 GAGGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 31

RESULT 37
US-09-969-373-613/c
Sequence 613, Application US/09969373
PATENT No. US2002013852A1
GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 613
LENGTH: 80
TYPE: DNA
ORGANISM: Glycine max
US-09-969-373-613

Query Match 0.4%; Score 22.2; DB 10; Length 80;
Best Local Similarity 56.0%; Pred. No. 1e+04; 33; Indels 0; Gaps 0;
Matches 42; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4036 GACATTAAGGTCACATATCTTACCTCATCTGATTATCAACCTGGAGATT 4095
DB 76 GAAATTAACCATCAATATATTATTATTATTATTATTATTATTATTATTATT 17
QY 4096 GGATGTCAGTAAG 4110
DB 16 TGATATTATTATTCAG 2

RESULT 38
US-09-864-761-22604
Sequence 22604, Application US/09864761
PATENT No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 24218
LENGTH: 75
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: MAP TO AC013746.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8

[illegible]

Query Match	0.48;	Score 22.2;	DB 10;	Length 86;
Best Local Similarity	64.7%;	Pred. No. 1.1e+04;		
Matches 33; Conservative	0;	Mismatches 18;	Indels 0;	Gaps 0;

RESULT 40
US-09-191

1 APPLICANT: Perrin, Marilyn H.
2 APPLICANT: Chen, Ruoping
3 APPLICANT: Lewis, Kathy A.
4 APPLICANT: Vale Jr., Wylie W.
5 APPLICANT: Donaldson, Cynthia J.
6 APPLICANT: Sachenko, Paul
7 TITLE OF INVENTION: Cloning and Recombinant Production of
8 TITLE OF INVENTION: CRE Receptor(s)
9 FILE APPROPRIATION: ()

```

? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)...(87)
? OTHER INFORMATION: CDS_R splice variant insert fragment
US-09-191-724-3

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Query Match	0.4%	Score 22.2	DB 10	Length 87
Best Local Similarity	61.0%	Pred. No. 1.1e+04		
Matches 36;	Conservative 0;	Mismatches 23;	Indels 0;	Gaps 0;
4620	GCTGCTCCTGTTTTCATGTGGCAAAAGGCCCTCGACGAGCGCTGCGGCACGAGT	4678		
5	GCTGACCCATTGGGGTGACCACGACCATGATGAGGCCCTGGAGAGGGGGCTCATTTAGAT	63		

Search completed: November 11, 2002, 12:43:10
Job time : 136 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 07:02:01 ; Search time 4213 Seconds
(without alignments)
19182.407 Million cell updates/sec

Title: US-09-676-436-3

Sequence: 1 ctgaagaattctccgatga.....ggttattttaagaagctc 4990

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357786

Minimum DB seq length: 8
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :
1: em_estba:*
2: em_estlum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_hlc:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_liv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39.8	0.8	95	AA990067	AA990067 ua58f02.r
2	30	0.6	64	17 DR12A12S	AL743114 Dapio.r
3	29	0.6	70	AA490364	AA490364 aa44c10.r
4	28.6	0.6	71	9 A1767078	A1767078 w192507.x
5	28	0.6	83	13 BU063432	BU063432 BU063432
6	27.8	0.6	17	BH863389	BH863389 SALK_0937

7	27.8	0.6	83	9 A1360096	A1360096 qb99d09.x
8	27.8	0.6	94	13 B1322285	B1322285 K139d08.r
9	27.8	0.6	100	14 A154655	A154655 mg61c08.r
10	27.4	0.5	91	14 T85845	T85845 yd61d10.r1
11	27.4	0.5	98	9 A1054386	A1054386 q176e03.x
12	26.8	0.5	88	9 AU254337	AU254337 AU254337
13	26.8	0.5	90	17 AL760836	AL760836 Arabidops
14	26.8	0.5	98	10 AV960997	AV960997 AV960997
15	26.8	0.5	100	14 C53310	C53310 C53310 Xu11
16	26.6	0.5	81	10 BE573242	BE573242 601331339
17	26.6	0.5	82	12 BF101686	BF101686 601753418
18	26.4	0.5	87	9 AA267457	AA267457 mz90a03.r
19	26.4	0.5	95	9 AA946634	AA946634 cq38f11.s
20	26.4	0.5	95	14 R93104	R93104 EST000038.S
21	26.2	0.5	78	14 R40354	R40354 YF81d05.s1
22	26.2	0.5	93	14 AV551027	AV551027 AV551027
23	26.2	0.5	78	14 T62011	T62011 YP97B12.r1
24	26.2	0.5	85	17 B1858071	B1858071 603384887
25	26	0.5	88	17 BH127076	BH127076 G-10924.f
26	26	0.5	88	17 AA865746	AA865746 oh41h1.s
27	26	0.5	88	17 AL757179	AL757179 Arabidops
28	26	0.5	88	17 A1251245	A1251245 qv55q12.x
29	25.8	0.5	78	9 A1033450	A1033450 ub47b05.x
30	25.8	0.5	83	9 AA915897	AA915897 OH86b08.s
31	25.8	0.5	91	9 A1340694	A1340694 LB33c02.x
32	25.8	0.5	91	9 A1894187	A1894187 mc67e06.x
33	25.8	0.5	100	9 AL794139	AL794139 AL794139
34	25.6	0.5	73	9 A1142956	A1142956 oz58d01.x
35	25.6	0.5	85	9 A1086378	A1086378 oz44c01.x
36	25.6	0.5	86	10 AV532477	AV532477 AV532477
37	25.6	0.5	87	17 AL754956	AL754956 Arabidops
38	25.4	0.5	79	10 AW149995	AW149995 XG32c06.x
39	25.4	0.5	89	14 A2961698	A2961698 2M0230B17
40	25.4	0.5	91	14 D19910	D19910 HMG500867
41	25.4	0.5	92	17 AF149669	AF149669 AF149669
42	25.4	0.5	93	17 AA659624	AA659624 ac20a02.s
43	25.4	0.5	94	9 AL662095	AL662095 AL662095
44	25.4	0.5	94	14 B0836143	B0836143 rf42d06.y
45	25.4	0.5	95	12 AA576542	AA576542 nm66c06.s
46	25.4	0.5	99	12 BG362479	BG362479 gb73a06.y
47	25.4	0.5	99	12 BF054677	BF054677 7169e05.y
48	25.2	0.5	64	10 AW626720	AW626720 SMOVAFCAP
49	25.2	0.5	68	17 A2574215	A2574215 326PVB08
50	25.2	0.5	81	9 AA451873	AA451873 x216e01.s
51	25.2	0.5	88	9 A1339161	A1339161 qf14h01.x
52	25.2	0.5	88	14 C01741	C01741 HMG5000363
53	25.2	0.5	94	13 B1943038	B1943038 sn03b04.y
54	25.2	0.5	97	17 TA330B01P	TA330B01P
55	25.2	0.5	98	14 NS0007	NS0007 yv24e01.r1
56	25	0.5	85	9 A1133686	A1133686 A3F Pyroc
57	25	0.5	86	9 A1539785	A1539785 tp7g05.x
58	25	0.5	90	9 AA831863	AA831863 ca59e04.s
59	25	0.5	100	9 A1080943	A1080943 BSHMFS21
60	24.8	0.5	78	9 H28412	H28412 y053f04.s1
61	24.8	0.5	82	9 AA922381	AA922381 oh91d11.s
62	24.8	0.5	82	9 AA888326	AA888326 nw73d04.s
63	24.8	0.5	82	12 BF533682	BF533682 602074086
64	24.8	0.5	93	9 A1000784	A1000784 AU007284
65	24.8	0.5	97	17 A2975978	A2975978 2M0251D16
66	24.8	0.5	98	14 B0742382	B0742382 Arabidops
67	24.8	0.5	100	17 A1764745	A1764745 Arabidops
68	24.6	0.5	68	14 B0524839	B0524839 NISC.nc07
69	24.6	0.5	92	9 AU267970	AU267970 AU267970
70	24.6	0.5	99	9 AA984185	AA984185 sm82a09.s
71	24.6	0.5	98	10 AV737113	AV737113
72	24.6	0.5	98	17 A2479591	A2479591 LM0300A30
73	24.6	0.5	100	13 R1052812	R1052812 RC4-GN03
74	24.6	0.5	100	14 B0394597	B0394597 NISC-ng10
75	24.4	0.5	68	17 CMS01Y5F	AL175572 Teladodon
76	24.4	0.5	70	13 BMS30543	BMS30543 IKS4f07.y
77	24.4	0.5	76	17 A2611518	A2611518 LM0437G19
78	24.4	0.5	75	17 AA922726	AA922726 ot84a12.s
79	24.4	0.5	95	12 BG256984	BG256984 602370A87

C 80	24.4	0.5	96	9	A1560569	A1560569 tq49b11.x	C 153	23.6	0.5	94	17	CNS033NU	AL226360 Telraodon
C 81	24.4	0.5	99	12	BF361342	BF361342 QV7-PT001	C 154	23.6	0.5	96	14	BQ381729	BQ381729 Kk45e09.y
C 82	24.4	0.5	100	9	A1152569	A1152569 udb8a03.r	C 155	23.6	0.5	97	17	A2366275	A2366275 1M01151b
C 83	24.4	0.5	100	9	A1681367	A1681367 lx46a03.r	C 156	23.6	0.5	97	17	A1864531	A1864531 w15a05.x
C 84	24.4	0.5	100	9	A1736172	A1736172 sb24c01.y	C 157	23.6	0.5	98	17	BH866271	BH866271 SALK_1009
C 85	24.4	0.5	100	9	AA623836	AA623836 vq69g02.s	C 158	23.6	0.5	98	17	CNS00XCA	AL094696 Arabidops
C 86	24.2	0.5	65	13	B05051122	B05051122 Bm051122	C 159	23.6	0.5	99	17	A2863592	A2863592 2M0171H09
C 87	24.2	0.5	67	9	A1222915	A1222915 qm29g05.x	C 160	23.6	0.5	100	9	AA855184	AA855184 aj33b12.s
C 88	24.2	0.5	78	12	BP238743	BP238743 601904328	C 161	23.6	0.5	100	9	A1499211	A1499211 t08e003.x
C 89	24.2	0.5	80	9	A1312379	A1312379 lca1c05.x	C 162	23.6	0.5	100	9	AU271250	AU271250 AU271250
C 90	24.2	0.5	83	9	A1611595	A1611595 l66f03.x	C 163	23.4	0.5	59	9	A1671994	A1671994 w02c06.x
C 91	24.2	0.5	84	10	AA675386	AA675386 bd45g09.y	C 164	23.4	0.5	73	9	A1670168	A2700117 2M038022
C 92	24.2	0.5	93	9	A1960759	A1960759 sc90a09.y	C 165	23.4	0.5	73	9	A1610168	A1610168 lpi3h08.x
C 93	24.2	0.5	93	9	AA411602	AA411602 zvi16g05.r	C 166	23.4	0.5	76	9	A1197096	A1197096 uds7d05.r
C 94	24.2	0.5	94	9	AA872482	AA872482 c110b07.s	C 167	23.4	0.5	77	9	AA789172	AA789172 ag58b09.s
C 95	24.2	0.5	94	9	A1397040	A1397040 fd25e03.y	C 168	23.4	0.5	78	17	AL768904	AL768904 Arabidops
C 96	24.2	0.5	94	9	A1611586	A1611586 l66e04.x	C 169	23.4	0.5	80	14	B0758288	B0758288 ERna03.SO
C 97	24.2	0.5	95	10	AV674632	AV674632 AV674632	C 170	23.4	0.5	81	14	C00156	C00156 HUMGS000579
C 98	24.2	0.5	96	10	BE246632	BE246632 NEF020B02L	C 171	23.4	0.5	84	13	BM435847	BM435847 lru544.ab
C 99	24.2	0.5	97	10	AM278082	AM278082 sf39e03.y	C 172	23.4	0.5	85	13	AA737424	AA737424 oa48d08.s
C 100	24.2	0.5	98	9	A1308454	A1308454 l64a10.x	C 173	23.4	0.5	86	13	BJ080960	BJ080960 BJ080960
C 101	24.2	0.5	98	9	A1540247	A1540247 l655b12.x	C 174	23.4	0.5	86	14	T82435	T82435 y02f04.s1
C 102	24.2	0.5	99	9	A1331232	A1331232 f898c01.y	C 175	23.4	0.5	87	9	AA546841	AA546841 vk67b02.s
C 103	24.2	0.5	56	17	B03428	B03428 GSR1-179A8	C 176	23.4	0.5	87	9	AA546841	AA546841 vk67b02.s
C 104	24.2	0.5	74	10	AV525712	AV525712 l31d11.x	C 177	23.4	0.5	89	10	AM302090	AM302090 x153d11.x
C 105	24.2	0.5	75	9	A1446279	A1446279 l31d11.x	C 178	23.4	0.5	90	17	BH216218	BH216218 1006041C0
C 106	24.2	0.5	81	17	BH849361	BH849361 SALK_0695	C 179	23.4	0.5	93	9	A1428297	A1428297 mm44g08.x
C 107	24.2	0.5	84	9	AA743463	AA743463 ny19c01.s	C 180	23.4	0.5	94	10	BE033377	BE033377 sm81a11.y
C 108	24.2	0.5	87	10	AV519819	AV519819 AV519819	C 181	23.4	0.5	95	9	A1142414	A1142414 q964h04.r
C 109	24.2	0.5	88	10	AV839096	AV839096 AV839096	C 182	23.4	0.5	96	9	A1336671	A1336671 q9w2e01.x
C 110	24.2	0.5	90	14	D34482	D34482 CELK046ESR	C 183	23.4	0.5	97	14	B0078719	B0078719 AU007819
C 111	24.2	0.5	93	13	BM157203	BM157203 lV45d12.y	C 184	23.4	0.5	97	17	A2402848	A2402848 EST 2655
C 112	24.2	0.5	94	9	AO267203	AO267203 2M0096K06	C 185	23.4	0.5	99	9	AA452857	AA452857 t12e603.x
C 113	24.2	0.5	96	17	AZ822902	AZ822902 2M0096K06	C 186	23.4	0.5	100	9	AA809558	AA809558 nj43d12.s
C 114	24.2	0.5	97	14	BQ455711	BQ455711 ke21h06.y	C 187	23.4	0.5	100	12	BF748792	BF748792 MR0-BN011
C 115	24.2	0.5	98	17	BH847422	BH847422 SALK_0531	C 188	23.4	0.5	100	14	BF751061	BF751061 MR0-BN011
C 116	24.2	0.5	99	13	BJ064494	BJ064494 SALK_0531	C 189	23.4	0.5	100	14	BQ397553	BQ397553 OH18G120
C 117	24.2	0.5	100	12	BF633479	BF633479 ve35d11.x	C 190	23.4	0.5	62	9	AL655180	AL655180 AL655180
C 118	24.2	0.5	51	17	B03367	B03367 GSR1-177B6	C 191	23.2	0.5	62	17	A2481769	A2481769 1M0306G13
C 119	23.8	0.5	64	10	AM626467	AM626467 SMOVAFARP	C 192	23.2	0.5	69	17	A2576681	A2576681 AST-TD1.4
C 120	23.8	0.5	64	10	AM626467	AM626467 SMOVAFARP	C 193	23.2	0.5	71	9	AA413615	AA413615 vcs7g04.s
C 121	23.8	0.5	72	17	AZ861143	AZ861143 SMOVAFARP	C 194	23.2	0.5	71	10	AA697232	AA697232 NF116E08S
C 122	23.8	0.5	72	17	AZ861143	AZ861143 SMOVAFARP	C 195	23.2	0.5	72	13	BI322719	BI322719 kx15d04.y
C 123	23.8	0.5	75	9	A1923606	A1923606 w175g12.x	C 196	23.2	0.5	72	13	BI322866	BI322866 kx09b07.y
C 124	23.8	0.5	84	14	B0548336	B0548336 rd24d09.y	C 197	23.2	0.5	74	13	BI322866	BI322866 kx13f05.y
C 125	23.8	0.5	87	9	AA533355	AA533355 ag65e01.s	C 198	23.2	0.5	75	13	BI322866	BI322866 kx12a10.y
C 126	23.8	0.5	88	14	BQ383621	BQ383621 NISC_mn02	C 199	23.2	0.5	75	13	BI322866	BI322866 kx12a10.y
C 127	23.8	0.5	88	14	BQ383621	BQ383621 NISC_mn02	C 200	23.2	0.5	80	13	BI742823	BI742823
C 128	23.8	0.5	90	14	T40328	T40328 yA32c06.r2	C 201	23.2	0.5	81	9	A1798074	A1798074 we84c11.x
C 129	23.8	0.5	92	9	AA178419	AA178419 m152e12.r	C 202	23.2	0.5	82	9	AA013827	AA013827 mh04g05.r
C 130	23.8	0.5	92	14	B0793758	B0793758 EST 2696	C 203	23.2	0.5	82	9	AA013827	AA013827 mh04g05.r
C 131	23.8	0.5	93	9	AA184929	AA184929 mu46f08.r	C 204	23.2	0.5	83	9	AA013827	AA013827 mh04g05.r
C 132	23.8	0.5	93	17	AZ440614	AZ440614 1M0231G15	C 205	23.2	0.5	84	13	BI451149	BI451149 kx11d01.r
C 133	23.8	0.5	97	9	A1383005	A1383005 lc21f12.x	C 206	23.2	0.5	84	13	BI451149	BI451149 kx11d01.r
C 134	23.8	0.5	99	10	AM600205	AM600205 SMLACAK11	C 207	23.2	0.5	85	13	BI742935	BI742935 kx36h01.y
C 135	23.8	0.5	100	17	AZ373796	AZ373796 1M0126G13	C 208	23.2	0.5	86	12	BB881724	BB881724 kx39h10.y
C 136	23.8	0.5	100	10	AV954067	AV954067 AV954067	C 209	23.2	0.5	86	12	BB881724	BB881724 kx39h10.y
C 137	23.6	0.5	59	14	C21189	C21189 HUMGS000220	C 210	23.2	0.5	87	13	BI742776	BI742776 kx34h11.y
C 138	23.6	0.5	69	9	AA388738	AA388738 vb22b03.r	C 211	23.2	0.5	88	13	BI742965	BI742965 kx37b11.y
C 139	23.6	0.5	73	12	BG310639	BG310639 SMOV3MCAM	C 212	23.2	0.5	88	13	BI742965	BI742965 kx37b11.y
C 140	23.6	0.5	76	9	AU012112	AU012112 AU012112	C 213	23.2	0.5	88	13	BI742965	BI742965 kx37b11.y
C 141	23.6	0.5	76	9	AU012112	AU012112 AU012112	C 214	23.2	0.5	89	13	BI742965	BI742965 kx37b11.y
C 142	23.6	0.5	77	9	A1564415	A1564415 tq74h04.x	C 215	23.2	0.5	90	9	AA910888	AA910888 kx39e05.y
C 143	23.6	0.5	81	14	B0759580	B0759580 HSPD1991.H	C 216	23.2	0.5	90	10	A1988876	A1988876 kx35b11.y
C 144	23.6	0.5	86	14	F29860	F29860 HSPD1991.H	C 217	23.2	0.5	90	10	AA910888	AA910888 kx35b11.y
C 145	23.6	0.5	87	9	AA231948	AA231948 AS31SB03	C 218	23.2	0.5	90	13	AA910888	AA910888 kx35b11.y
C 146	23.6	0.5	88	17	AL757787	AL757787 Arabidops	C 219	23.2	0.5	91	9	AA065987	AA065987 kx34h09.y
C 147	23.6	0.5	89	17	AZ303890	AZ303890 1M0030P10	C 220	23.2	0.5	92	9	AA065987	AA065987 kx34h09.y
C 148	23.6	0.5	89	17	BH408514	BH408514 1007004A0	C 221	23.2	0.5	93	12	BF322806	BF322806 maa33h11.x
C 149	23.6	0.5	91	17	AZ322634	AZ322634 1M0043P04	C 222	23.2	0.5	93	17	BH223849	BH223849 1006115D0
C 150	23.6	0.5	93	9	AA488835	AA488835 aa34h10.r	C 223	23.2	0.5	94	9	BH812090	BH812090 SALK_0511
C 151	23.6	0.5	93	17	BH846992	BH846992 SALK_0125	C 224	23.2	0.5	94	9	A1664252	A1664252 ue60e12.r
C 152	23.6	0.5	94	17	CNS020IM	AL209335 Telraodon	C 225	23.2	0.5	95	14	BQ393535	BQ393535 NISC_mg04

226	23.2	0.5	95	14	H98130	H98130 yx10d06.sl	299	22.8	0.5	88	9	A1252396	A1252396 qv28h10.x
227	23.2	0.5	95	17	A2623818	A2623818 1M0461H19	300	22.8	0.5	89	10	BE318823	BE318823 NF066602L
228	23.2	0.5	96	17	A2650879	A2650879 2M0215P16	301	22.8	0.5	89	12	BE318828	BE318828 NF066604P
229	23.2	0.5	98	10	A2651886	A2651886 1O205B03-	302	22.8	0.5	90	1	A1988276	A1988276 sc98d12.y
230	23.2	0.5	98	13	BM343075	BM343075 fw51c06.y	303	22.8	0.5	90	14	BO754116	BO754116 EBB301-SQ
231	23.2	0.5	99	10	AV852688	AV852688 AV852688	304	22.8	0.5	90	17	AL752638	AL752638 AtadIdops
232	23.2	0.5	99	10	BE166843	BE166843 CM2-HT050	305	22.8	0.5	91	14	AA663819	AA663819 aer7f01.s
233	23.2	0.5	99	14	T50985	T50985 yb71d01.sl	306	22.8	0.5	91	14	BQ255855	BQ255855 NISC-1q06
234	23.2	0.5	99	17	TA242A060	TA242A060	307	22.8	0.5	92	14	AL679606	AL679606 AL679606
235	23.2	0.5	100	17	A1882508	A1882508 ubd7a08.1	308	22.8	0.5	92	10	AV531478	AV531478 AV531478
236	23.2	0.5	100	12	BE874679	BE874679 CM0-ET012	309	22.8	0.5	92	13	BI335801	BI335801 42-12.Hum
237	23.2	0.5	103	10	AV533029	AV533029 AV533029	310	22.8	0.5	93	9	A1096771	A1096771 qa06h07.x
238	23.2	0.5	65	13	BJ049547	BJ049547 BJ049547	311	22.8	0.5	93	9	A1620635	A1620635 tu47h10.x
239	23.2	0.5	69	9	AA589335	AA589335 vm36g05.t	312	22.8	0.5	94	9	AT004331	AT004331 AT004331
240	23.2	0.5	71	17	A2471347	A2471347 1M0285121	313	22.8	0.5	94	10	AV966686	AV966686 AV966686
241	23.2	0.5	72	13	AI638207	AI638207 ts97f107.x	314	22.8	0.5	94	10	AM189645	AM189645
242	23.2	0.5	77	13	BI962533	BI962533 1e51d07.y	315	22.8	0.5	98	9	A1340472	A1340472
243	23.2	0.5	78	9	AI988368	AI988368 sdt01a03.y	316	22.8	0.5	98	17	AU270324	AU270324
244	23.2	0.5	80	17	CNS02YWM	AL216329 Tetradon	317	22.8	0.5	98	17	AZ785762	AZ785762 1M0030A02
245	23.2	0.5	81	17	A2479949	A2479949 1M0301J06	318	22.8	0.5	99	12	BG153740	BG153740 naq59c02.r
246	23.2	0.5	82	17	AA171633	AA171633 z094a06.x	319	22.8	0.5	99	14	R76313	R76313 y123e12.r1
247	23.2	0.5	82	17	AA504005	AA504005 nh39f05.s	320	22.8	0.5	100	10	AV921214	AV921214 AV921214
248	23.2	0.5	83	10	AM086303	AM086303 xc71g06.s	321	22.8	0.5	100	12	BE687936	BE687936 CM1-IT004
249	23.2	0.5	83	10	AA040005	AA040005 1M0172J01	322	22.8	0.5	100	14	BQ380842	BQ380842 kx31e06.y
250	23.2	0.5	86	17	AA442749	AA442749 zvg6a11.s	323	22.8	0.5	100	17	CNS01XC7	CNS01XC7
251	23.2	0.5	88	14	HI9431	HI9431 yma6g11.sl	324	22.8	0.5	37	9	AI302081	AI302081 qv57e12.x
252	23.2	0.5	88	17	HSEXTK35	HSEXTK35	325	22.8	0.5	56	10	AV519485	AV519485
253	23.2	0.5	89	17	AI364393	AI364393 qw37b04.x	326	22.8	0.5	57	12	BG099228	BG099228 naq8d11.
254	23.2	0.5	90	13	BI782005	BI782005 K104C03.y	327	22.8	0.5	59	10	AV519835	AV519835 AV519835
255	23.2	0.5	91	9	AI366782	AI366782 q941d10.x	328	22.8	0.5	62	17	A2477006	A2477006 1M0296E17
256	23.2	0.5	92	17	A2346732	A2346732 1M0082B07	329	22.8	0.5	64	13	BI142468	BI142468 SMOV3KCM
257	23.2	0.5	92	17	AI804741	AI804741 tu42c05.x	330	22.8	0.5	67	12	BE383386	BE383386 602045048
258	23.2	0.5	93	13	BJ039041	BJ039041 BJ039041	331	22.8	0.5	69	13	BI219526	BI219526 602936603
259	23.2	0.5	93	13	R85951	R85951 yf66c04.sl	332	22.8	0.5	71	9	BI779137	BI779137 EBr001-SQ
260	23.2	0.5	94	9	AI088953	AI088953 cu86b05.s	333	22.8	0.5	79	13	AA661918	AA661918 nc67b04.x
261	23.2	0.5	94	9	AI179326	AI179326 as40d02.x	334	22.8	0.5	72	14	BM706635	BM706635 UI-E-COD-
262	23.2	0.5	96	9	AI901286	AI901286 sc31e03.y	335	22.8	0.5	75	9	AA689902	AA689902 v62h12.r
263	23.2	0.5	96	10	AM191884	AM191884 x17e108.x	336	22.8	0.5	76	17	A2968712	A2968712 2M0241K10
264	23.2	0.5	96	10	BQ235155	BQ235155 hds4f04.g	337	22.8	0.5	77	17	BH864548	BH864548 SALK-0962
265	23.2	0.5	96	17	B32145	B32145 HS-1014-B2-	338	22.8	0.5	79	9	AI180073	AI180073 tm71h05.x
266	23.2	0.5	97	9	AL803618	AL803618 AL803618	339	22.8	0.5	79	9	AI688144	AI688144
267	23.2	0.5	97	9	AL061738	AL061738 AU061738	340	22.8	0.5	79	10	AI250495	AI250495 AV558917
268	23.2	0.5	97	10	BE652631	BE652631 UI-M-AQ1-	341	22.8	0.5	80	9	AI690691	AI690691 AV558917
269	23.2	0.5	97	14	BO127273	BO127273 1157h11.y	342	22.8	0.5	80	9	AI250495	AI250495 v425a08.x
270	23.2	0.5	97	14	BQ68250	BQ68250 sap44e12.	343	22.8	0.5	80	9	AI690691	AI690691 v425a08.x
271	23.2	0.5	98	14	AI439550	AI439550 fb36c04.y	344	22.8	0.5	81	9	AI250495	AI250495 v425a08.x
272	23.2	0.5	98	10	AM516362	AM516362 xy9g11.x	345	22.8	0.5	81	9	AI250495	AI250495 v425a08.x
273	23.2	0.5	98	10	AM516362	AM516362 xy9g11.x	346	22.8	0.5	81	9	AI250495	AI250495 v425a08.x
274	23.2	0.5	99	13	BI557423	BI557423 603338225	347	22.8	0.5	81	17	A2421879	A2421879
275	23.2	0.5	99	13	BI557423	BI557423 603338225	348	22.8	0.5	82	10	BE282088	BE282088
276	23.2	0.5	100	9	AA736635	AA736635 sb31c05.y	349	22.8	0.5	82	9	AA180875	AA180875
277	23.2	0.5	100	9	AA736635	AA736635 sb31c05.y	350	22.8	0.5	84	9	AI685692	AI685692
278	23.2	0.5	100	9	AA736635	AA736635 sb31c05.y	351	22.8	0.5	85	9	AI685692	AI685692
279	23.2	0.5	100	13	BI033614	BI033614 PM1-NH120	352	22.8	0.5	85	14	T61535	T61535
280	23.2	0.5	54	9	AI564489	AI564489 tq57h12.x	353	22.8	0.5	86	9	AI470691	AI470691
281	23.2	0.5	67	14	NA1028	NA1028 yv53c05.sl	354	22.8	0.5	86	9	AI470691	AI470691
282	23.2	0.5	68	17	AZ474039	AZ474039 1M0290G16	355	22.8	0.5	86	10	AV534836	AV534836
283	23.2	0.5	69	10	AM698388	AM698388 G234.g1an	356	22.8	0.5	87	10	AV519786	AV519786
284	23.2	0.5	69	17	AL760933	AL760933 ArabIdops	357	22.8	0.5	87	10	AV532625	AV532625
285	23.2	0.5	69	17	CNS02WBC	AL216849 Tetradon	358	22.8	0.5	87	17	AL761571	AL761571
286	23.2	0.5	70	17	AZ796084	AZ796084 2M0051G04	359	22.8	0.5	88	10	AV563877	AV563877
287	23.2	0.5	71	13	BI736720	BI736720 603360414	360	22.8	0.5	89	9	AU007252	AU007252
288	23.2	0.5	76	17	AA260720	AA260720 val12h09.r	361	22.8	0.5	89	14	BO090826	BO090826
289	23.2	0.5	76	17	AL756306	AL756306 ArabIdops	362	22.8	0.5	91	9	AA014022	AA014022
290	23.2	0.5	77	14	F32860	F32860 HSPD25935.H	363	22.8	0.5	91	10	AV519886	AV519886
291	23.2	0.5	79	12	AI223775	AI223775 qx32f02.x	364	22.8	0.5	92	10	AV760647	AV760647
292	23.2	0.5	82	9	BF031392	BF031392 601559175	365	22.8	0.5	92	10	AV760647	AV760647
293	23.2	0.5	82	9	AA510767	AA510767 ar77b05.x	366	22.8	0.5	92	10	AV760647	AV760647
294	23.2	0.5	85	9	AA804737	AA804737 of48a08.s	367	22.8	0.5	92	14	R72581	R72581
295	23.2	0.5	85	9	AA935761	AA935761 on13f11.s	368	22.8	0.5	94	9	AI433403	AI433403
296	23.2	0.5	85	9	AA404572	AA404572 z141b03.r	369	22.8	0.5	94	9	AA47086	AA47086
297	23.2	0.5	86	17	BH227411	BH227411 1006139H0	370	22.8	0.5	94	14	R26640	R26640
298	23.2	0.5	87	17	AI251224	AI251224 qv39g12.x	371	22.8	0.5	95	10	AV519671	AV519671

C 372	22.6	0.5	95	17	A2659464	A2659464 IM0536A22	C 445	22.4	0.4	100	12	Bf087192	Bf087192 RC3-HT047
C 373	22.6	0.5	96	14	AA212521	AA212521 mw77D06.r	C 446	22.4	0.4	100	13	Bj435259	Bj435259 B435259
C 374	22.6	0.5	96	14	N21324	N21324 yx49a11.s1	C 447	22.4	0.4	100	14	Bm733732	Bm733732 K42508.Y
C 375	22.6	0.5	96	14	N27632	N27632 yw50c05.s1	C 448	22.2	0.4	45	9	AU258887	AU258887
C 376	22.6	0.5	96	17	BH405867	BH405867 RPCI-23-8	C 449	22.2	0.4	53	17	BH609802	BH609802
C 377	22.6	0.5	97	12	Bf148426	Bf148426 uy80h09.x	C 450	22.2	0.4	59	9	AA414865	AA414865
C 378	22.6	0.5	98	9	A1193808	A1193808 qe59g04.x	C 451	22.2	0.4	64	9	AA413891	AA413891 vc71c04.s
C 379	22.6	0.5	98	13	B1259645	B1259645 602968541	C 452	22.2	0.4	64	9	AA473691	AA473691 vq93a04.r
C 380	22.6	0.5	98	17	A2769905	A2769905 1M0571H05	C 453	22.2	0.4	64	12	Bf400453	Bf400453 vq65a02.r
C 381	22.6	0.5	99	14	H38793	H38793 ynb3g06.r1	C 454	22.2	0.4	69	13	AU269389	AU269389 SMOVL3CAN
C 382	22.6	0.5	100	12	A1105878	A1105878 cb04g10.p	C 455	22.2	0.4	65	13	B1676701	B1676701 tcs3c01.x
C 383	22.6	0.5	100	12	Bf815228	Bf815228 MR2-C1012	C 456	22.2	0.4	70	17	A2694534	A2694534 AST-ZH8BG
C 384	22.6	0.5	100	13	Bj086513	Bj086513 Bf086513	C 457	22.2	0.4	70	17	CNS02E3X	AL192524 TelradP05
C 385	22.4	0.4	58	17	B00351	B00351 CSR1-108a2-	C 458	22.2	0.4	72	12	B6673201	B6673201 DNNBP05
C 386	22.4	0.4	54	17	A2499503	A2499503 IM0337M13	C 459	22.2	0.4	74	10	AV832572	AV832572 AV832572
C 387	22.4	0.4	63	14	BQ243213	BQ243213 TAE15017G	C 460	22.2	0.4	74	17	A2490565	A2490565 IM033A09
C 388	22.4	0.4	67	9	A1538304	A1538304 tp6th10.x	C 461	22.2	0.4	75	14	BH810491	BH810491 SALK_0497
C 389	22.4	0.4	70	10	Bf681222	Bf681222 dq08a06.Y	C 462	22.2	0.4	75	14	AA903811	AA903811 OK56g11.s
C 390	22.4	0.4	72	9	AA500503	AA500503 v181g05.r	C 463	22.2	0.4	75	14	B0523783	B0523783 NISC_n124
C 391	22.4	0.4	73	9	A161934	A161934 tdl8a10.x	C 464	22.2	0.4	76	9	A1335738	A1335738 CH35e02.x
C 392	22.4	0.4	74	14	BQ795066	BQ795066 EST 4004	C 465	22.2	0.4	78	14	C02363	C02363 HUMGS000931
C 393	22.4	0.4	74	14	BQ795066	BQ795066 EST 4427	C 466	22.2	0.4	78	17	A2381260	A2381260 t00137P12
C 394	22.4	0.4	76	14	B0541350	B0541350 p63g07.Y	C 467	22.2	0.4	79	9	A1537245	A1537245 t001f03.x
C 395	22.4	0.4	76	17	DR10N4S	DR10N4S ret	C 468	22.2	0.4	79	14	BQ266862	BQ266862 NISC_f115
C 396	22.4	0.4	77	14	BQ795490	BQ795490 EST 4428	C 469	22.2	0.4	80	14	AV851139	AV851139 AV851139
C 397	22.4	0.4	77	17	BH851619	BH851619 SALK_0732	C 470	22.2	0.4	80	14	F34720	F34720 HSPD29811 H
C 398	22.4	0.4	78	17	BH851619	BH851619 SALK_0990	C 471	22.2	0.4	81	9	AU007999	AU007999 AU007999
C 399	22.4	0.4	79	14	BQ793571	BQ793571 EST 2509	C 472	22.2	0.4	81	10	AM323780	AM323780 u076e01.Y
C 400	22.4	0.4	79	17	BH405787	BH405787 RPCI-23-2	C 473	22.2	0.4	81	14	F337841	F337841 HSPD26374 H
C 401	22.4	0.4	81	10	AV953855	AV953855 AV953855	C 474	22.2	0.4	82	9	A1377841	A1377841 t63g01.x
C 402	22.4	0.4	83	9	A1505128	A1505128 vq69g02.x	C 475	22.2	0.4	83	9	AA671672	AA671672 v105d05.r
C 403	22.4	0.4	83	9	AU255693	AU255693 A255693	C 476	22.2	0.4	83	9	A1869444	A1869444 t441a11.x
C 404	22.4	0.4	83	12	BG058145	BG058145 mah21c04.	C 477	22.2	0.4	84	12	BG203583	BG203583 RST22967
C 405	22.4	0.4	84	14	Bm733743	Bm733743 k125d03.Y	C 478	22.2	0.4	85	17	A2434086	A2434086 IM0220M17
C 406	22.4	0.4	85	10	BE058925	BE058925 sm22g05.Y	C 479	22.2	0.4	86	12	BG234263	BG234263 daa39a09
C 407	22.4	0.4	87	9	AU257147	AU257147 AU257147	C 480	22.2	0.4	86	12	W52422	W52422 t014f08.x
C 408	22.4	0.4	88	9	AA027165	AA027165 z63g02.s	C 481	22.2	0.4	86	14	W52422	W52422 t014f08.x
C 409	22.4	0.4	88	9	A1384188	A1384188 tdl7108.Y	C 482	22.2	0.4	86	14	W52422	W52422 t014f08.x
C 410	22.4	0.4	88	13	AA566535	AA566535 ZF-ES56.Z	C 483	22.2	0.4	86	14	W52422	W52422 t014f08.x
C 411	22.4	0.4	88	13	BM397269	BM397269 5009-0-30	C 484	22.2	0.4	87	17	BH800773	BH800773
C 412	22.4	0.4	88	14	BQ795230	BQ795230 EST 4168	C 485	22.2	0.4	87	17	A1539781	A1539781 t00128D0
C 413	22.4	0.4	89	17	A2587910	A2587910 IM0395119	C 486	22.2	0.4	87	17	AF038532	AF038532 AF038532
C 414	22.4	0.4	89	17	A2587910	A2587910 IM0395119	C 487	22.2	0.4	88	17	A2628049	A2628049
C 415	22.4	0.4	91	9	AA952854	AA952854 SHMBCA00	C 488	22.2	0.4	89	13	A1918394	A1918394
C 416	22.4	0.4	91	9	A1988660	A1988660 sc06b10.Y	C 489	22.2	0.4	89	10	AM026944	AM026944
C 417	22.4	0.4	91	14	N85628	N85628 J4211F.Huma	C 490	22.2	0.4	90	13	B1493480	B1493480
C 418	22.4	0.4	91	17	AL760481	AL760481 Arabidops	C 491	22.2	0.4	91	17	A2345951	A2345951
C 419	22.4	0.4	92	9	A1784233	A1784233 tw58b01.x	C 492	22.2	0.4	91	17	A2345951	A2345951
C 420	22.4	0.4	93	9	AA502077	AA502077 pg72b07.s	C 493	22.2	0.4	92	17	A2373615	A2373615
C 421	22.4	0.4	94	9	A1987884	A1987884 um08c10.x	C 494	22.2	0.4	92	13	B1257458	B1257458
C 422	22.4	0.4	94	9	AA205202	AA205202 zq71n06.s	C 495	22.2	0.4	92	17	A2378719	A2378719
C 423	22.4	0.4	94	9	AA215618	AA215618 zt95e06.r	C 496	22.2	0.4	93	17	A2602030	A2602030
C 424	22.4	0.4	95	9	AA279608	AA279608 zs88b02.r	C 497	22.2	0.4	93	9	A1331231	A1331231
C 425	22.4	0.4	95	14	BQ793588	BQ793588 EST 2526	C 498	22.2	0.4	93	17	A2626144	A2626144
C 426	22.4	0.4	95	14	W11427	W11427 ma90b07.r1	C 499	22.2	0.4	94	9	A1330911	A1330911
C 427	22.4	0.4	95	17	A2779171	A2779171 2M0015M12	C 500	22.2	0.4	94	14	N33799	N33799
C 428	22.4	0.4	96	9	AA823928	AA823928 vq93a05.r	C 501	22.2	0.4	94	14	AL634796	AL634796
C 429	22.4	0.4	96	9	AJ500170	AJ500170 AJ500170	C 502	22.2	0.4	95	14	AA174188	AA174188
C 430	22.4	0.4	96	13	Bj031535	Bj031535 Bf031535	C 503	22.2	0.4	95	14	N86930	N86930
C 431	22.4	0.4	97	9	AA247813	AA247813 hfe0676.s	C 504	22.2	0.4	95	17	CNS0321G	CNS0321G
C 432	22.4	0.4	97	13	B1979207	B1979207 f188e05.x	C 505	22.2	0.4	96	9	A1442889	A1442889
C 433	22.4	0.4	97	13	B1979207	B1979207 f188e05.x	C 506	22.2	0.4	96	14	AA583853	AA583853
C 434	22.4	0.4	98	9	AU2673504	AU2673504 A26767030	C 507	22.2	0.4	96	14	F32461	F32461
C 435	22.4	0.4	98	9	AU2673504	AU2673504 A26767030	C 508	22.2	0.4	96	14	W67624	W67624
C 436	22.4	0.4	98	10	AV956469	AV956469 AV956469	C 509	22.2	0.4	97	9	AA666986	AA666986
C 437	22.4	0.4	98	14	H13520	H13520 y115b09.s1	C 510	22.2	0.4	97	9	AL820194	AL820194
C 438	22.4	0.4	98	17	BH814666	BH814666 SALK_0667	C 511	22.2	0.4	97	9	BM096718	BM096718
C 439	22.4	0.4	99	10	AM302439	AM302439 xrt46h09.x	C 512	22.2	0.4	97	13	AL754186	AL754186
C 440	22.4	0.4	99	12	BG894372	BG894372 xrt46h09.x	C 513	22.2	0.4	97	17	AU053647	AU053647
C 441	22.4	0.4	99	17	AZ802736	AZ802736 xrt46h09.x	C 514	22.2	0.4	98	10	AA459323	AA459323
C 442	22.4	0.4	100	9	AA127365	AA127365 zn91h09.r	C 515	22.2	0.4	99	14	B0457368	B0457368
C 443	22.4	0.4	100	10	AM065297	AM065297 614045E02	C 516	22.2	0.4	99	17	B36233	B36233
C 444	22.4	0.4	100	12	Bf680992	Bf680992 602156276	C 517	22.2	0.4	99	17	B36233	B36233

C 518	22.2	0.4	99	17	BH615045	BH615045 KG00582-5	591	22	0.4	100	13	B1942718	B1942718 sk79e03.y
C 519	22.2	0.4	100	9	AI617512	AI617512 zehnl705.	592	22	0.4	100	13	B1024186	B1024186 B1024186
C 520	22.2	0.4	100	9	AI988516	AI988516 s003d03.y	593	22	0.4	100	13	B1432532	B1432532 B1432532
C 521	22.2	0.4	100	9	AUI79053	AUI79053 AUI79053	594	22	0.4	100	13	B1432532	B1432532 B1432532
C 522	22.2	0.4	100	9	AA529357	AA529357 v135908.r	595	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 523	22.2	0.4	100	9	AA624889	AA624889 vnr33908.r	596	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 524	22.2	0.4	100	12	BG258990	BG258990 602379012	597	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 525	22.2	0.4	100	12	BG258990	BG258990 602379012	598	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 526	22.2	0.4	100	13	BI001519	BI001519 PM1-UT006	599	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 527	22.2	0.4	100	17	AL768524	AL768524 Arpbldops	600	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 528	22.2	0.4	55	17	AA649524	AA649524 1M0519C09	601	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 529	22.2	0.4	64	17	AA085966	AA085966 z183h12.s	602	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 530	22.2	0.4	62	14	BH756304	BH756304 SALK_0534	603	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 531	22.2	0.4	79	17	BH756304	BH756304 P1EStoab1	604	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 532	22.2	0.4	73	10	AI739189	AI739189 w127c11.x	605	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 533	22.2	0.4	73	10	AA626517	AA626517 SMOVI3CAN	606	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 534	22.2	0.4	73	10	AA626517	AA626517 SMOVI3CAN	607	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 535	22.2	0.4	73	10	AA626517	AA626517 SMOVI3CAN	608	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 536	22.2	0.4	74	17	BH857828	BH857828 SALK_0874	609	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 537	22.2	0.4	74	17	CNS04HAT	AI290702 Tetracodon	610	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 538	22.2	0.4	75	10	AA615120	AA615120 vn02b09.r	611	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 539	22.2	0.4	75	10	AA615120	AA615120 vn02b09.r	612	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 540	22.2	0.4	77	10	BE320162	BE320162 NF025H03R	613	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 541	22.2	0.4	77	12	BG885255	BG885255 dac38d04.	614	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 542	22.2	0.4	77	14	BO456810	BO456810 ke31c12.y	615	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 543	22.2	0.4	77	14	DI2050	DI2050 HMM051807	616	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 544	22.2	0.4	77	14	AL738069	AL738069 Arabldops	617	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 545	22.2	0.4	78	10	AV949979	AV949979 AV949979	618	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 546	22.2	0.4	79	10	AV844464	AV844464 AV844464	619	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 547	22.2	0.4	79	17	CNS0206U	AI208901 Tetracodon	620	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 548	22.2	0.4	80	9	AI469588	AI469588 lml4a07.x	621	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 549	22.2	0.4	80	14	T24433	T24433 EST008 Huma	622	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 550	22.2	0.4	80	17	AA2580217	AA2580217 1M0568F19	623	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 551	22.2	0.4	82	9	AI754536	AI754536 lT04911.x	624	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 552	22.2	0.4	82	9	AI754536	AI754536 lT04911.x	625	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 553	22.2	0.4	83	14	BO569882	BO569882 g1138c11.	626	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 554	22.2	0.4	84	17	BO391586	AI765680 NTC_mq19	627	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 555	22.2	0.4	85	17	AL765680	AI765680 Arabldops	628	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 556	22.2	0.4	86	17	AA107738	AA107738 mc48e04.r	629	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 557	22.2	0.4	86	17	AZ591254	AZ591254 1M0401F17	630	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 558	22.2	0.4	87	17	AA506305	AA506305 nh45a08.s	631	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 559	22.2	0.4	88	17	BH857820	BH857820 SALK_0874	632	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 560	22.2	0.4	88	12	AI130113	AI130113 z135D09.s	633	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 561	22.2	0.4	88	12	BG152617	BG152617 na157h09.	634	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 562	22.2	0.4	88	13	BM027222	BM027222 kt92a03.y	635	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 563	22.2	0.4	88	13	BM027222	BM027222 kt92a03.y	636	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 564	22.2	0.4	88	17	BH848705	BH848705 SALK_0687	637	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 565	22.2	0.4	91	9	AI933472	AI933472 vnr4a04.x	638	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 566	22.2	0.4	92	17	BH858238	AI933472 vnr4a04.x	639	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 567	22.2	0.4	92	17	BH858238	BH858238 SALK_0831	640	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 568	22.2	0.4	93	17	AI782700	AI782700 g183h07.x	641	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 569	22.2	0.4	93	17	AI782700	AI782700 g183h07.x	642	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 570	22.2	0.4	94	12	AI909296	AI909296 602409941	643	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 571	22.2	0.4	94	12	BG391993	BG391993 602409941	644	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 572	22.2	0.4	95	9	AI014994	AI014994 602409941	645	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 573	22.2	0.4	96	13	BI499032	BI499032 1e28g09.x	646	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 574	22.2	0.4	97	9	AA714476	AA714476 1e28g09.x	647	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 575	22.2	0.4	97	9	AA714476	AA714476 1e28g09.x	648	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 576	22.2	0.4	97	12	BG057467	BG057467 na18h05.	649	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 577	22.2	0.4	97	12	BG057467	BG057467 na18h05.	650	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 578	22.2	0.4	98	10	AA190110	AA190110 m181e08.r	651	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 579	22.2	0.4	98	10	AA190110	AA190110 m181e08.r	652	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 580	22.2	0.4	98	12	BF651089	BF651089 NF101A01E	653	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 581	22.2	0.4	98	14	TF62017	TF62017 yb97c10.r1	654	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 582	22.2	0.4	98	14	TF62017	TF62017 yb97c10.r1	655	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 583	22.2	0.4	99	9	AI988193	AI988193 sc96d07.y	656	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 584	22.2	0.4	99	9	AA619313	AA619313 vp13g12.r	657	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 585	22.2	0.4	99	10	AA619313	AA619313 vp13g12.r	658	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 586	22.2	0.4	100	9	AA013690	AA013690 mh07h11.r	659	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 587	22.2	0.4	100	9	AA013690	AA013690 mh07h11.r	660	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 588	22.2	0.4	100	9	AA342827	AA342827 EST48417	661	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 589	22.2	0.4	100	13	BI003554	BI003554 MR3-HN012	662	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 590	22.2	0.4	100	13	BI024076	BI024076 CM3-MT035	663	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 591	22.2	0.4	100	13	BI024076	BI024076 CM3-MT035	664	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 592	22.2	0.4	100	13	BI024076	BI024076 CM3-MT035	665	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 593	22.2	0.4	100	13	BI024076	BI024076 CM3-MT035	666	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 594	22.2	0.4	100	13	BI024076	BI024076 CM3-MT035	667	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 595	22.2	0.4	100	13	BI024076	BI024076 CM3-MT035	668	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 596	22.2	0.4	100	13	BI024076	BI024076 CM3-MT035	669	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 597	22.2	0.4	100	13	BI024076	BI024076 CM3-MT035	670	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 598	22.2	0.4	100	13	BI024076	BI024076 CM3-MT035	671	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 599	22.2	0.4	100	13	BI024076	BI024076 CM3-MT035	672	21.8	0.4	100	13	B1432532	B1432532 B1432532
C 600	22.2	0.4	100	13	BI024076	BI024076 CM3-MT035							

C 664	21.8	0.4	93	9	AU013433	AU013433	AU013433	C 737	21.6	0.4	82	13	B3055136	B3055136
C 665	21.8	0.4	93	13	BM445282	BM445282	BM445282	C 738	21.6	0.4	83	9	AA680618	AA680618
C 666	21.8	0.4	93	14	BM879727	BM879727	BM879727	C 739	21.6	0.4	83	9	AA814174	AA814174
C 667	21.8	0.4	93	14	BQ234543	BQ234543	BQ234543	C 740	21.6	0.4	83	10	AA639304	AA639304
C 668	21.8	0.4	93	14	BQ386012	BQ386012	BQ386012	C 741	21.6	0.4	84	9	AA591819	AA591819
C 669	21.8	0.4	93	14	BQ788232	BQ788232	BQ788232	C 742	21.6	0.4	84	13	BA137764	BA137764
C 670	21.8	0.4	93	17	AZ305460	AZ305460	AZ305460	C 743	21.6	0.4	85	9	AA637555	AA637555
C 671	21.8	0.4	93	17	BH128522	BH128522	BH128522	C 744	21.6	0.4	85	9	AU265253	AU265253
C 672	21.8	0.4	94	9	AL1016972	AL1016972	AL1016972	C 745	21.6	0.4	85	14	BM955050	BM955050
C 673	21.8	0.4	94	10	AL836084	AL836084	AL836084	C 746	21.6	0.4	86	17	AZ380924	AZ380924
C 674	21.8	0.4	94	12	BE908034	BE908034	BE908034	C 747	21.6	0.4	87	14	BE881724	BE881724
C 675	21.8	0.4	94	14	BQ788464	BQ788464	BQ788464	C 748	21.6	0.4	87	17	N34848	N34848
C 676	21.8	0.4	94	17	AZ479471	AZ479471	AZ479471	C 749	21.6	0.4	87	17	AZ780952	AZ780952
C 677	21.8	0.4	95	14	W89778	W89778	W89778	C 750	21.6	0.4	88	9	AA068421	AA068421
C 678	21.8	0.4	95	17	AZ576188	AZ576188	AZ576188	C 751	21.6	0.4	88	9	AU046593	AU046593
C 679	21.8	0.4	95	17	AL763855	AL763855	AL763855	C 752	21.6	0.4	88	10	BE325908	BE325908
C 680	21.8	0.4	95	17	CNS0608X	CNS0608X	CNS0608X	C 753	21.6	0.4	88	17	AZ956706	AZ956706
C 681	21.8	0.4	96	9	AA766618	AA766618	AA766618	C 754	21.6	0.4	89	9	AA403229	AA403229
C 682	21.8	0.4	96	9	AL868116	AL868116	AL868116	C 755	21.6	0.4	89	9	AA483286	AA483286
C 683	21.8	0.4	96	9	AT883268	AT883268	AT883268	C 756	21.6	0.4	89	12	BG910719	BG910719
C 684	21.8	0.4	96	17	AZ427959	AZ427959	AZ427959	C 757	21.6	0.4	89	17	AL756274	AL756274
C 685	21.8	0.4	97	9	AI930887	AI930887	AI930887	C 758	21.6	0.4	89	17	AL756274	AL756274
C 686	21.8	0.4	97	9	AA179461	AA179461	AA179461	C 759	21.6	0.4	89	17	AL756274	AL756274
C 687	21.8	0.4	97	10	AA678563	AA678563	AA678563	C 760	21.6	0.4	89	17	AL756274	AL756274
C 688	21.8	0.4	97	10	AA678563	AA678563	AA678563	C 761	21.6	0.4	90	2	HSMD03105	HSMD03105
C 689	21.8	0.4	97	14	CA84172	CA84172	CA84172	C 762	21.6	0.4	90	12	BG153212	BG153212
C 690	21.8	0.4	97	17	BH849830	BH849830	BH849830	C 763	21.6	0.4	91	14	BQ126492	BQ126492
C 691	21.8	0.4	97	17	TA105B01P	TA105B01P	TA105B01P	C 764	21.6	0.4	91	12	BG562086	BG562086
C 692	21.8	0.4	98	9	AJ500931	AJ500931	AJ500931	C 765	21.6	0.4	91	12	BG562086	BG562086
C 693	21.8	0.4	98	13	BI492384	BI492384	BI492384	C 766	21.6	0.4	91	13	BM068861	BM068861
C 694	21.8	0.4	98	13	BJ047711	BJ047711	BJ047711	C 767	21.6	0.4	91	17	AZ824717	AZ824717
C 695	21.8	0.4	98	17	BH848162	BH848162	BH848162	C 768	21.6	0.4	92	17	BH813191	BH813191
C 696	21.8	0.4	99	9	AJ500079	AJ500079	AJ500079	C 769	21.6	0.4	92	17	BH813191	BH813191
C 697	21.8	0.4	99	17	BH863371	BH863371	BH863371	C 770	21.6	0.4	92	17	BH813191	BH813191
C 698	21.8	0.4	100	9	AA683899	AA683899	AA683899	C 771	21.6	0.4	93	10	AL797662	AL797662
C 699	21.8	0.4	100	9	AI767200	AI767200	AI767200	C 772	21.6	0.4	93	10	AU099097	AU099097
C 700	21.8	0.4	100	10	AA436968	AA436968	AA436968	C 773	21.6	0.4	93	14	BQ235010	BQ235010
C 701	21.8	0.4	100	12	BE906284	BE906284	BE906284	C 774	21.6	0.4	93	17	AZ848413	AZ848413
C 702	21.8	0.4	100	12	BE906284	BE906284	BE906284	C 775	21.6	0.4	94	9	AA727090	AA727090
C 703	21.8	0.4	100	13	BI491202	BI491202	BI491202	C 776	21.6	0.4	94	9	AA1201345	AA1201345
C 704	21.8	0.4	100	13	BM090987	BM090987	BM090987	C 777	21.6	0.4	94	9	AA106067	AA106067
C 705	21.8	0.4	100	13	BM090987	BM090987	BM090987	C 778	21.6	0.4	94	9	AA106067	AA106067
C 706	21.8	0.4	100	13	BM090987	BM090987	BM090987	C 779	21.6	0.4	94	9	AA106067	AA106067
C 707	21.8	0.4	100	13	BM090987	BM090987	BM090987	C 780	21.6	0.4	94	9	AA106067	AA106067
C 708	21.8	0.4	100	13	BM090987	BM090987	BM090987	C 781	21.6	0.4	94	9	AA106067	AA106067
C 709	21.8	0.4	100	13	BM090987	BM090987	BM090987	C 782	21.6	0.4	94	13	BM42762	BM42762
C 710	21.8	0.4	100	13	BM090987	BM090987	BM090987	C 783	21.6	0.4	95	12	BF225188	BF225188
C 711	21.6	0.4	100	17	TH339604Q	TH339604Q	TH339604Q	C 784	21.6	0.4	95	17	AZ576154	AZ576154
C 712	21.6	0.4	55	12	BG153530	BG153530	BG153530	C 785	21.6	0.4	96	9	AU008340	AU008340
C 713	21.6	0.4	55	12	BG153530	BG153530	BG153530	C 786	21.6	0.4	96	9	AU008340	AU008340
C 714	21.6	0.4	55	14	H14140	H14140	H14140	C 787	21.6	0.4	96	14	BQ636146	BQ636146
C 715	21.6	0.4	57	17	B03689	B03689	B03689	C 788	21.6	0.4	97	9	AZ854992	AZ854992
C 716	21.6	0.4	58	9	AI473789	AI473789	AI473789	C 789	21.6	0.4	97	9	A1036529	A1036529
C 717	21.6	0.4	58	17	AZ656081	AZ656081	AZ656081	C 790	21.6	0.4	97	9	A1255137	A1255137
C 718	21.6	0.4	59	9	AI880479	AI880479	AI880479	C 791	21.6	0.4	97	9	A1321720	A1321720
C 719	21.6	0.4	63	13	BI412820	BI412820	BI412820	C 792	21.6	0.4	97	9	A1540563	A1540563
C 720	21.6	0.4	64	9	AA522905	AA522905	AA522905	C 793	21.6	0.4	97	12	BF434734	BF434734
C 721	21.6	0.4	66	9	AA522905	AA522905	AA522905	C 794	21.6	0.4	97	17	AZ514087	AZ514087
C 722	21.6	0.4	67	9	AA191154	AA191154	AA191154	C 795	21.6	0.4	97	17	CNS0251V	CNS0251V
C 723	21.6	0.4	68	9	AI139634	AI139634	AI139634	C 796	21.6	0.4	97	17	CNS048VQ	CNS048VQ
C 724	21.6	0.4	70	9	AA922430	AA922430	AA922430	C 797	21.6	0.4	98	12	BF593054	BF593054
C 725	21.6	0.4	70	14	W58297	W58297	W58297	C 798	21.6	0.4	98	14	BG175207	BG175207
C 726	21.6	0.4	73	9	AU256317	AU256317	AU256317	C 799	21.6	0.4	98	14	BQ393450	BQ393450
C 727	21.6	0.4	73	9	AA397711	AA397711	AA397711	C 800	21.6	0.4	98	17	N51544	N51544
C 728	21.6	0.4	74	17	AZ854180	AZ854180	AZ854180	C 801	21.6	0.4	98	17	AU073033	AU073033
C 729	21.6	0.4	75	10	AA696083	AA696083	AA696083	C 802	21.6	0.4	99	10	BE4303078	BE4303078
C 730	21.6	0.4	75	10	AA696083	AA696083	AA696083	C 803	21.6	0.4	99	12	BG170557	BG170557
C 731	21.6	0.4	77	10	AA696083	AA696083	AA696083	C 804	21.6	0.4	99	13	BI813983	BI813983
C 732	21.6	0.4	77	10	AA696083	AA696083	AA696083	C 805	21.6	0.4	99	14	BM935438	BM935438
C 733	21.6	0.4	77	17	AA696083	AA696083	AA696083	C 806	21.6	0.4	99	14	BM935438	BM935438
C 734	21.6	0.4	79	10	AA696083	AA696083	AA696083	C 807	21.6	0.4	99	17	AZ756344	AZ756344
C 735	21.6	0.4	79	13	BI746313	BI746313	BI746313	C 808	21.6	0.4	99	17	AZ756344	AZ756344
C 736	21.6	0.4	82	9	AA260536	AA260536	AA260536	C 809	21.6	0.4	99	17	AL770229	AL770229

C 810	21.6	0.4	100	9	A1254756	qV53a01.x	C 883	21.4	0.4	87	17	CNS01700	A1166761	Retradon
C 811	21.6	0.4	100	9	A1307456	lB34c03.x	C 884	21.4	0.4	87	17	CNS026DH	A1183230	Retradon
C 812	21.6	0.4	100	9	A1611770	lU79409.x	C 885	21.4	0.4	88	9	A0566472	A0666472	m173a0.x
C 813	21.6	0.4	100	9	AL820525	AL820525	C 886	21.4	0.4	88	9	A1154895	A1154895	u277b05.x
C 814	21.6	0.4	100	10	AM306738	s147901.y	C 887	21.4	0.4	88	9	A1581205	A1581205	lv70e05.x
C 815	21.6	0.4	100	10	AM579660	PM2-H7022	C 888	21.4	0.4	88	14	B0693077	B0693077	N5CSC.ng01
C 816	21.6	0.4	100	10	BE681958	179807.MA	C 889	21.4	0.4	88	14	T956818	T956818	y454508.s1
C 817	21.6	0.4	100	12	BF830753	CM3-H7096	C 890	21.4	0.4	88	17	AZ313668	AZ313668	lM0030FE24
C 818	21.6	0.4	100	12	BG266854	1000107A0	C 891	21.4	0.4	88	17	AZ313667	AZ313667	2M01951118
C 819	21.6	0.4	100	12	BG735862	rk47f02.y	C 892	21.4	0.4	89	12	BE629357	BE629357	6016563118
C 820	21.6	0.4	100	12	BE771162	RC5-F7007	C 893	21.4	0.4	89	12	BE320493	BE320493	u253h03.y
C 821	21.6	0.4	100	17	AZ575720	AST-T73A0	C 894	21.4	0.4	89	14	B0793650	B0793650	EST_2588
C 822	21.6	0.4	100	17	AZ808703	2M0072D19	C 895	21.4	0.4	89	17	AZ324243	AZ324243	lM0246EB09
C 823	21.6	0.4	50	9	AU108026	AU108026	C 896	21.4	0.4	89	17	AZ448190	AZ448190	lM0246A817
C 824	21.4	0.4	52	13	BM307184	sak37g12-	C 897	21.4	0.4	90	9	AZ6768167	AZ6768167	lM0556H05
C 825	21.4	0.4	53	13	BT701611	sa117h07.	C 898	21.4	0.4	90	10	AV845095	AV845095	AV845095
C 826	21.4	0.4	56	17	AZ33942	lM0045H10	C 899	21.4	0.4	90	10	AV845095	AV845095	AV845095
C 827	21.4	0.4	56	17	BH865702	SAIK_0997	C 900	21.4	0.4	90	14	AM696910	AM696910	NFL112E03S
C 828	21.4	0.4	57	13	AU265867	AU265867	C 901	21.4	0.4	90	14	W52603	W52603	zC9C0C1.r1
C 829	21.4	0.4	57	13	B1158906	B1158906	C 902	21.4	0.4	91	17	BH408358	BH408358	lS067001A0
C 830	21.4	0.4	58	9	A1339339	qT01h12.x	C 903	21.4	0.4	91	10	AM423611	AM423611	sh69001A0
C 831	21.4	0.4	61	9	A1630615	a413c06.x	C 904	21.4	0.4	91	12	BG495369	BG495369	602539670
C 832	21.4	0.4	61	12	BM368412	qB68c05.y	C 905	21.4	0.4	91	13	H1867608	H1867608	lE51d01.y
C 833	21.4	0.4	64	9	AU2688231	AU2688231	C 906	21.4	0.4	91	17	AZ438806	AZ438806	lM0229M06
C 834	21.4	0.4	64	10	BE588255	SMOYPMCAQ	C 907	21.4	0.4	92	13	AA792063	AA792063	vN69c10.r
C 835	21.4	0.4	66	14	BQ479327	K32h12.y	C 908	21.4	0.4	92	13	BI073731	BI073731	k134b11.y
C 836	21.4	0.4	67	14	N44602	yl13e04.r1	C 909	21.4	0.4	92	14	BM897793	BM897793	pH43c02.y
C 837	21.4	0.4	70	9	A1687087	lP4B04.x	C 910	21.4	0.4	93	14	BM898110	BM898110	ph59e07.y
C 838	21.4	0.4	70	17	CNS035YW	CNS035YW	C 911	21.4	0.4	93	14	B0382559	B0382559	lM0246C03
C 839	21.4	0.4	71	9	AA915904	oH8c08.s	C 912	21.4	0.4	94	14	BM444477	BM444477	lRT04C03
C 840	21.4	0.4	72	9	AA624405	vN03f06.r	C 913	21.4	0.4	94	14	BM431019	BM431019	k855c02.y
C 841	21.4	0.4	72	14	BQ625446	r415p01.y	C 914	21.4	0.4	94	12	BF014866	BF014866	sa29h09.y
C 842	21.4	0.4	73	12	BG087913	H314d05-	C 915	21.4	0.4	94	13	BI321008	BI321008	rat24a10.
C 843	21.4	0.4	74	9	AI217246	qT74b10.x	C 916	21.4	0.4	95	14	BM897618	BM897618	ph36c04.y
C 844	21.4	0.4	74	14	N67765	za02909.s1	C 917	21.4	0.4	95	14	AA656765	AA656765	vF07f12.r
C 845	21.4	0.4	74	17	AZ463167	lM0271n14	C 918	21.4	0.4	95	14	BM897667	BM897667	ph36h11.y
C 846	21.4	0.4	74	17	AZ566798	z26PvE09	C 919	21.4	0.4	95	17	R86088	R86088	y062h03.r1
C 847	21.4	0.4	74	17	AZ938802	2M0197F04	C 920	21.4	0.4	95	17	AZ472761	AZ472761	lM0288M08
C 848	21.4	0.4	74	17	BA2030	HS-1055-A1-	C 921	21.4	0.4	95	17	AZ813261	AZ813261	2M0081B03
C 849	21.4	0.4	75	10	AV969420	AV969420	C 922	21.4	0.4	96	9	AL800435	AL800435	AL800435
C 850	21.4	0.4	75	10	AV969420	AV969420	C 923	21.4	0.4	96	12	RC271892	RC271892	na154e10.
C 851	21.4	0.4	75	14	BO541016	ps75f109.y	C 924	21.4	0.4	96	12	BM897185	BM897185	ph57d07.y
C 852	21.4	0.4	75	17	AZ813424	2M0080N12	C 925	21.4	0.4	96	14	BM812788	BM812788	SAIK_0631
C 853	21.4	0.4	76	9	AU269382	AU269382	C 926	21.4	0.4	97	13	AM569446	AM569446	s187c02.y
C 854	21.4	0.4	76	10	AA470550	x285f01.x	C 927	21.4	0.4	97	10	BM895946	BM895946	ph559450
C 855	21.4	0.4	76	17	AZ868330	2M0180F03	C 928	21.4	0.4	97	13	BI079735	BI079735	6028763232
C 856	21.4	0.4	77	10	BE023551	smB2a04.y	C 929	21.4	0.4	97	13	BI200231	BI200231	nl1601fs.r
C 857	21.4	0.4	77	17	AZ776504	2M0010K11	C 930	21.4	0.4	97	14	H25068	H25068	Y131c03.r1
C 858	21.4	0.4	79	9	AA915843	SMOYL3CAN	C 931	21.4	0.4	97	14	U398134	U398134	CS038134.FD
C 859	21.4	0.4	79	9	AA967284	AA967284	C 932	21.4	0.4	97	14	Z19805	Z19805	HSMAARVC
C 860	21.4	0.4	79	9	AU010116	AU010116	C 933	21.4	0.4	98	14	EM897050	EM897050	ph55905.y
C 861	21.4	0.4	79	10	AAW646530	cm65h09.w	C 934	21.4	0.4	98	14	BM897052	BM897052	ph55907.y
C 862	21.4	0.4	79	12	BC939282	602411486	C 935	21.4	0.4	98	14	A1666501	A1666501	fd16e930.x
C 863	21.4	0.4	79	14	BO248557	TaE25007D	C 936	21.4	0.4	99	9	AU258290	AU258290	AU258290
C 864	21.4	0.4	79	14	D11626	HUM0C13G12	C 937	21.4	0.4	99	9	AA247766	AA247766	nl6e0473.s
C 865	21.4	0.4	79	17	BH411610	1007033C0	C 938	21.4	0.4	99	10	AV919754	AV919754	AV919754
C 866	21.4	0.4	80	9	AU077289	AU077289	C 939	21.4	0.4	99	10	AV954727	AV954727	AV954727
C 867	21.4	0.4	80	10	AM023871	dfe1b08.y	C 940	21.4	0.4	99	10	AW150368	AW150368	x950e05.x
C 868	21.4	0.4	81	17	A1388836	qW15c08.x	C 941	21.4	0.4	99	10	AM171420	AM171420	l141d05.x
C 869	21.4	0.4	81	17	AZ353256	lM0092E10	C 942	21.4	0.4	99	10	AM867620	AM867620	MRO-SN003
C 870	21.4	0.4	82	9	A1371451	rT56c12.x	C 943	21.4	0.4	99	10	BE323458	BE323458	NFO0E03P
C 871	21.4	0.4	82	9	AA601116	nc54k12.x	C 944	21.4	0.4	99	10	BE323458	BE323458	NFO0E03P
C 872	21.4	0.4	82	17	TA501D08Q	T_brucel	C 945	21.4	0.4	99	12	BG796928	BG796928	UTSW-SM6H
C 873	21.4	0.4	83	9	AA106395	l19o610.r	C 946	21.4	0.4	99	14	BO275108	BO275108	p141c10.y
C 874	21.4	0.4	83	12	BF013315	rk32a02.y	C 947	21.4	0.4	99	14	BO275108	BO275108	p141c10.y
C 875	21.4	0.4	84	12	BF137937	601784f03	C 948	21.4	0.4	99	17	BH633548	BH633548	g136e07.y
C 876	21.4	0.4	84	17	AZ321360	lM0041L18	C 949	21.4	0.4	99	17	BM633820	BM633820	SAIK_0432
C 877	21.4	0.4	84	17	BH813900	SAIK_0634	C 950	21.4	0.4	99	17	CNS02APY	CNS02APY	AL188863
C 878	21.4	0.4	85	9	AU013959	AU013959	C 951	21.4	0.4	99	17	TA535026P	TA535026P	AL497121
C 879	21.4	0.4	86	9	A1299562	qN11h08.x	C 952	21.4	0.4	100	10	BE090225	BE090225	RC0-TB071
C 880	21.4	0.4	86	13	BI496152	d1123b08.	C 953	21.4	0.4	100	10	BE164523	BE164523	RC3-HT047
C 881	21.4	0.4	87	9	AA968122	uN11912.r	C 954	21.4	0.4	100	10	BE578337	BE578337	rk10h06.y
C 882	21.4	0.4	87	10	AW546822	L0013D11-	C 955	21.4	0.4	100	12	BF772272	BF772272	CM4-TT004

```

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseestev@son.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGe Consortium (info@image.llnl.gov) for further information.
MGI:699731
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 82.

FEATURES
Source
1..95
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1361691"
/clone_lib="Soares_thymus_2nbm"
/sex="male"
/tissue_type="thymus"
/lab_stage="4 weeks"
/lab_host="DH10B"
(note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTATCAATCTGAAGTGGAGCGCGCGTGTGTTTTTTTTTTTTTTTTTTT
3'], double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT3D vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fátima Bonaldo.")
BASE COUNT      27 a      19 c      26 g      23 t
ORIGIN
Query Match      0.8%; Score 39.8; DB 9; Length 95;
Best Local Similarity 70.7%; Pred. No. 14;
Matches 53; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
OY 4471 GAATGACCCGTAAGTATGATGAAATTCCTTATACACTACTATGATATA 4530
      ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 16 GAACGACCCGCTAGCTAGCTGTGTGACAGAAATCCGATGACACTATGATATA 75
OY 4531 TTTACATAAAGACTG 4545
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db TTTACATAAAGACTG 90

```

LOCUS	DR12A125	64 bp	DNA	linear	GSS 06-JUN-2002
DEFINITION	Danio rerio genomic clone DKey-12A12,				genomic survey sequence.
ACCESSION	AL743114				
VERSION	AL743114.1	GI:21340560			
KEYWORDS	GSS.				
SOURCE	zebrafish.				
ORGANISM	Danio rerio				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Actinopterygii; Neopterygii; Teleostei; Ostariophysi;				
	Cypriniformes; Cyprinidae; Danio.				
	1 (bases 1 to 64)				
REFERENCE	Humphray, S.J., Huckle, E. and Hunt, S.E.				
AUTHORS	Direct Submission				
TITLE	Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome				
JOURNAL	Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:				
	humquerry@sanger.ac.uk Unpublished				
COMMENT	This sequence was generated from the SP6 end of BAC 12A12. 12A12 is				
	part of the Daniokey Pilot BAC Library created by R. Plasterk and				
	N.V. Keygene				
FEATURES	Further details: http://www.sanger.ac.uk/projects/D_rerio/ .				
source	location/Qualifiers				
	1. 64				
	/organism="Danio rerio"				
	/db_xref="taxon:7955"				
	/c1one="DKey-12A12"				

[illegible]


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/clone="IMAGE:2019185"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/notes="Organ: Brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I oligo(dT) primer (5'
TCTTCCATCTGAAGTGGAGGCGCCGACATAGGTTTCTTTTCTTTTCTTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73D vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaudo."

BASE COUNT      19 a      6 c      4 g      54 t
ORIGIN
Query Match      0.6%   Score 27.8; DB 9; Length 83;
Best Local Similarity 59.5%   Pred. No. 2.6e+04;
Matches 47; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 475 TTTGAACTTACAGCTTTGTAAGCTTACCTCACTCAAGAAAAAGACAGAGAG 534
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 83 TTTAAAAATTTTAAATTTCTTAAGTCACTTGGCTTTAAGAAAAAAGAAAAA 24
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 535 CAAGAGGACAGAAAAA 553
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 23 AAAAAAAGAAAAA 5
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
BI322285 94 bp mRNA linear EST 30-JUL-2001
LOCUS kx19a08.y3 Parastromyloides trichosuri FL PAMPI v1 Chapeli
DEFINITION McCarter Parastromyloides trichosuri cDNA 5', mRNA sequence.
ACCESSION BI322285.1 GI:15001471
VERSION EST
KEYWORDS Parastromyloides trichosuri.
SOURCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
ORGANISM Panagrolaimidae; Strongyloidea; Parastromyloides.
REFERENCE 1 (bases 1 to 94)
AUTHORS McCarter, D., Clifton, S., Chapeli, B., Pape, D., Martin, J., Wylie, T.,
Dante, M., Maier, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,
Gibbons, M., Ritzer, E., Bennett, J., Franklin, C., Tsagaris, V., R.,
Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe,
M., Allen, M., Person, B., Swales, T., Harvey, N., Schurk, K., Kohn, S.,
Shin, T., Jackson, T., Cardenas, M., McCann, K., Waterston, R. and
Wilson, R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
The library was constructed by Brandi Chapeli and Dr. James
McCarter (bchapel@wustl.wustl.edu & jmcarter@wustl.wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
putative full length read
The vector to vector length is 95
Seq primer: -40RP from Gibco.
FEATURES
Source
1..94
location/Qualifiers
/organism="Parastromyloides trichosuri"
/db_xref="taxon:131310"
/clone_lib="Parastromyloides trichosuri FL PAMPI v1
Chapeli McCarter"
/dev_stage="free living"
/lab_host="DH10B"
/lab_stage="DH10B"

/clone="Vector: PAMPI (Gibco); Site_1: NotI; Site_2: SalI;
The library was constructed by Brandi Chapeli and Dr.
James McCarter at Washington University, St. Louis. The
cDNA was made by using Dynabead oligo-dT priming (Dynal).
PCR based library using a modified protocol from the
SMART PCR cDNA synthesis kit from Clontech. Directionally
cloned into the UDG sites of PAMPI. Nematodes were
provided by Dr. Warwick Grant of AgResearch, New Zealand
(warwick.grant@agresearch.co.nz)."

BASE COUNT      42 a      9 c      12 g      31 t
ORIGIN
Query Match      0.6%   Score 27.8; DB 13; Length 94;
Best Local Similarity 62.0%   Pred. No. 2.7e+04;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 3542 AGAAGTCAGTCCGATTTGTAAGAAAGAGTCCGGAAGAGAGAGAAATATCA 3601
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8 AAAATTACATCCAGTCAATGAAATAAAGACATCAAAAAAGAGCTGTATATATTT 67
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3602 TTGGTCAAGTT 3612
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 68 TTTATCAAGTT 78
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
AA154655/c
LOCUS AA154655
DEFINITION
ACCESSION AA154655.1 GI:1726483
VERSION EST
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Maier, M., Hillier, L., Allen, M., Bowers, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maier M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:357862
Trace considered overall poor quality
possible reversed clone; similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
FEATURES
Source
1..100
location/Qualifiers
/organism="Mus musculus"
/strain="57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:363214"
/clone_lib="Soares_thymus_2NBMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/lab_stage="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

```


Query Match	0.5%	Score 26.4	DB 9	Length 95
Best Local Similarity	59.2%	Pred. No. 6.5e+04		
Matches	45; Conservative	0; Mismatches	31; Indels	0; Gaps
QY 4876	CCTTTACCTTTTGTGTTGTGGCAAGCTGCAGGTTTGTAATGCAGAAAGCGTGATAC			4935
Db 92	CTTTTACTTTGTGTAATTTGTGAGTTTCAGAAAGACTTTTTTTTAAAAAAATAAAGTCCCTAC			33
QY 4936	TGAAATTTAAGAAAAA	4951		
Db 32	TTACACTTAATAAAAAA	17		

RESULT 20	
R93104	
LOCUS	95 bp mRNA linear EST 28-AUG-1995
DEFINITION	ES0000038.5. manson1 cDNA Schistosoma mansoni
ACCESSION	SW678485.1
VERSION	R93104
KEYWORDS	GI:965458
SOURCE	EST
ORGANISM	Schistosoma mansoni
	Schistosoma mansoni
	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
REFERENCE	Strigileddi; Schistosomatidae; Schistosomatidae; Schistosoma.
	1 (bases 1 to 95)
AUTHORS	Saber, M.A., Hamied, H., Elyassaki, W.M., Romeih, M., Ahmed, H., Mohareb
	, M., Eldaba, I., and Mandouh, S.
TITLE	Schistosoma mansoni cDNAs
JOURNAL	Unpublished (1995)
COMMENT	Contact: M.A. Saber, H. Hamied, W.M. El Yassaki, M. Romeih, H.

```

FEATURES
  source          location/Qualifiers
1. .95
Seq primer: sk.
build: M-Sabder@RCU.EON.EG

```

BASE COUNT	31 a	15 c	10 g	39 t
ORIGIN				

Query Match	Similarity	0.53;	Score 26.4;	DB 14;	Length 95;
Best local	Similarity	59.28;	Pred. No. 6.5e+04;		
Matches	45;	Conservative	0;	Mismatches 31;	Indels 0;
					Gaps 0;
641	ACTCTCTTTATATACAGCCGTCACAGCCATCCGATATATTATTAACAAATCCTTACTT	700			
b	5 ACTATGATTATTATTAACACTGATTCACGACATCCCTTATCTATTAATAAGTATCTTATT	64			
y	701 TCAAGTCGACTATGG	716			
d	65 TGAATTTTACCATAG	80			

RESULT	21
R40354/c	
LOCUS	
DEFINITION	78 bp mRNA linear EST 05-MAY-1995
ACCESION	Y81805.s1 Soares infant brain INIB Homo sapiens cDNA clone
VERSION	R40354
KEYWORDS	R40354.1 GI:797970
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 78)
TITLE	Hillier,L., Clark,N., Dubouque,T., Elliston,K., Hawkins,M., Holman .M., Hulthman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,B., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston .R., Williamson,A., Woldmann,P. and Wilson,R.
JOURNAL	The WashU-Wercx EST Project
COMMENT	Unpublished (1995)
CONTACT:	Contact: Wilson RK

High quality sequence stop: 48.
Seq primer: Promega -21m13
Insert Length: 2347 Std Error: 0.00
Consortium (info@image.llnl.gov) for further information.
High quality sequence stops: 61 Source: IMAGE Consortium. LLNL This
clone is available royalty-free through LLNL ; contact the IMAGE

```

source
1. 78
/organism="Homo sapiens"
/db_xref="GBR:401364"
/db_xref="taxon:9606"
/clone="IMAGE:29017"
/clone_1fb="Soares Infant brain IN1B"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: whole brain; Vector: lafmid BA; Site: 1: Not
I; Site: 2: Hind III; 1st strand cDNA was primed with a Not
I - Oligo(dT) primer [5,
ACTGTGAGATATTCGCGCCGACAGAAATTTT TTTT TTTT TTTT TTTT
3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the lafmid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
7 a 5 c 7 g 57 t 2 others

```

Query Match	0.58;	Score 26.2;	DB 14;	Length 78;
Best Local Similarity	64.9%;	Pred. No. 6.9e+04;		
Matches 37;	Conservative	0;	Mismatches 20;	Indels 0;
0Y	498	AAAGCTTACCTCAGTCTCAAGAAAAAGACAGGAGCAAGAGACAGAAAAATTC	554	

Query Match
 Best Local Similarity 59.5%; Score 26; DB 13; Length 78;
 Matches 44; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

19 a 19 c 23 g 17 t

BASE COUNT
 19 a 19 c 23 g 17 t

ORIGIN

Query Match
 Best Local Similarity 59.5%; Score 26; DB 13; Length 78;
 Matches 44; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

19 a 19 c 23 g 17 t

BASE COUNT
 19 a 19 c 23 g 17 t

ORIGIN

RESULT 25
 LOCUS BH127076/c 85 bp DNA linear GSS 23-JUL-2001
 DEFINITION G-10g24.f Maize Random Small-Insert Genomic Library Zea mays
 ACCESSION BH127076
 VERSION BH127076.1 GI:14994908
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 1 (bases 1 to 85)
 REFERENCE Meyers, B.C., Tingey, S.V. and Morgante, M.
 Abundance, distribution and transcriptional activity of repetitive
 elements in the maize genome
 Genome Res. 11 (10), 1660-1676 (2001)
 JOURNAL MEDLINE
 COMMENT 21475670
 Contact: Morgante M
 Suite 200
 Dupont Genomics
 PO Box 6104, Newark, DE 19714-6104, USA
 Tel: 302 631 2638
 Fax: 302 631 2607
 Email: Michele.morgante@usa.dupont.com
 Sequences were trimmed to include only high quality bases; forward
 and reverse reads were assembled when significant overlaps were
 detected.
 Seq primer: M13univ
 Class: Shotgun

FEATURES
 source

Location/Qualifiers
 1..85
 /organism="Zea mays"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_id="G-10g24"
 /clone_lib="Maize Random Small-Insert Genomic Library"
 /sex="hermaphrodite"
 /tissue_type="leaf"
 /cell_type="young leaf"
 /dev_stage="seedling"
 /note="Vector: PCR-Script; Total genomic DNA was nebulized
 ; ends were polished with pfu polymerase and the fragments
 cloned into PCR-Script."
 BASE COUNT
 20 a 18 c 11 g 36 t

ORIGIN

Query Match
 Best Local Similarity 57.3%; Score 26; DB 17; Length 85;
 Matches 47; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

19 a 19 c 23 g 17 t

BASE COUNT
 19 a 19 c 23 g 17 t

ORIGIN

RESULT 26
 LOCUS AA865746 88 bp mRNA linear EST 13-MAY-1998
 DEFINITION Oth1h1.s1 NCI_CGAP_G4 Homo sapiens CDNA clone IMAGE:1469253 3',
 mRNA sequence.
 ACCESSION AA865746
 VERSION AA865746.1 GI:2958022
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 88)
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 Tissue procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 2310 Std Error: 0.00
 Seq primer: 40m13 fwd. ET from Amersham
 High quality sequence stop: 51.
 Location/Qualifiers
 1..88
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="NCI_CGAP_G4"
 /clone_lib="NCI_CGAP_G4"
 /tissue_type="Pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from 3 pooled
 germ cell tumors, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73
 vector. Library is normalized. Library was constructed by
 Bento Soares and M. Fatima Bonaldo."

FEATURES
 source

Location/Qualifiers
 1..85
 /organism="Homo sapiens"
 /strain="B73"
 /db_xref="taxon:9606"
 /clone_id="NCI_CGAP_G4"
 /clone_lib="NCI_CGAP_G4"
 /tissue_type="Pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from 3 pooled
 germ cell tumors, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73
 vector. Library is normalized. Library was constructed by
 Bento Soares and M. Fatima Bonaldo."
 BASE COUNT
 31 a 10 c 13 g 34 t

Query Match
 Best Local Similarity 62.1%; Score 26; DB 9; Length 88;
 Matches 41; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

19 a 19 c 23 g 17 t

BASE COUNT
 19 a 19 c 23 g 17 t

ORIGIN

This clone is available royalty-free through the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:903317
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 63.
 Location/Qualifiers

FEATURES
source

1. .78

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1360849"
/clone_lib="Sources_mammary_gland_NBIMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
lab_host="DH10B"

```

BASE COUNT	23 a	13 c	24 g	18 t
ORIGIN				

Query Match	0.5%	Score 25.8;	DB 9;	Length 78;
Best Local Similarity	60.9%;	Pred. No. 8.8e+04;		
Matches	42;	Conservative	0;	Mismatches 27;
				Indels 0;

QY	3514	TCGAACCTGGACCCATAGAACCTCTCCAGAAAGTCAGTCGCATTTGTTTGAAGAAAGAGG	3573
Db	3	TGTTAAACACGGCCACACAGATGTTTTTCAGATGCGCTTCCTTTGGGCGAAGAGGAGAAAT	62
QY	3574	TACCGAGAA	3582
Db	63	TGGCGAGAA	71

RESULT 30	
AA915897	
LOCUS	83 bp MRNA linear EST 14-APR-1996
DEFINITION	Osh8bB08.s1 NCI_CGAP_CoB Homo sapiens CDNA clone IMAGE:1473879 3'
	sequence.
ACCESSION	AA915897
VERSION	AA915897.1 GI:3055289
KEYWORDS	EST.
SOURCE	human.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDDA Tissue Bank

FEATURES

CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.linnl.gov/bdip/image/image.html
Seq primer: -40ml3 fwd. RT from Amersham.
Location/Qualifiers

source

1.83

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1473879"
/clone_lib="NCI CGAP_Cc8"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT7T3D-Pac (pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento, Soares and M. Fatima Bonaldo."

```

BASE COUNT	32 a	14 c	8 g	29 t
ORIGIN				

Query Match	0.58;	Score 25.8;	DB 9;	Length 83;
Best Local Similarity	58.48;	Pred. No. 9.1e+04;		
Matches 45; Conservative		0; Mismatches 32;		Indels

QY	1899	GTATTTTCATTTACATGACAGCTGCGATCCAAATGCTACAGCAATTAACCTCAGCATGCA	1958
Db	6	GTTTATGATTTATTATTAACTTGTGGACCAAAAATAAACCAATTAACCAACCATGCT	65
QY	1959	TACTTTAAAAATCTGT	1975
Db	66	TACTTATCAAAATGTAT	82

RESULT 31	
AI340694	
LOCUS	
DEFINITION	91 bp mRNA
AI340694	tb53c05.x1 NCI_CGAP_B:15 Homo sapiens CDNA clone IMAGE:2058056 3'
	similar to gb:U059897.fml ALZHEIMER S DISEASE AMYLOID A4 PROTEIN
	PRECURSOR (HUMAN);', mRNA sequence.
AI340694	
ACCESSION	
VERSION	AI340694.1 GI:4077621
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 91)	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	Unpublished (1997)
			Unpublished (1997)	Contact: Robert Strausberg Ph D

Email: cgaphbs-remail.mh.gov
 Tissue Procurement: Dennis Segol, M.D., Kristina Cole, M.D., Ph.D.
 student, Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Krizman, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdpr/image/image.html
 Insert length: 164 Std Error: 0.00
 Seq primer: -400bp from Gibco.

FEATURES
source

Location/Qualifiers
1. .91

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2058056"
/clone_lib="NCI_CGAP_Brl5"
/sex="female"
/tissue_type="adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: breast; Vector: pAMP1; mRNA made from breast
adenocarcinoma tissue, cDNA made by oligo-dT priming.

```

directionally cloned. Size-selected on agarose gel,
average insert size 400 bp. Primary library,
non-amplified."

BASE COUNT 39 a 7 c 35 g 10 t
ORIGIN
Query Match 0.5%; Score 25.8; DB 9; Length 91;
Best Local Similarity 58.4%; Pred. No. 9.4e+04;
Matches 45; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

RESULT 32
A1894187/c 91 bp mRNA linear EST 27-JUN-1999
LOCUS
DEFINITION
m67e06.x1 Soares mouse embryo NDME13.5 14.5 Mus musculus CDNA
clone IMAGE:353602 3' similar to SW:RPB2_HUMAN P30876 DNA-DIRECTED
RNA POLYMERASE II 140 KD POLYPEPTIDE ; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 91)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Stephens, M., Rheising, B., Allen, M., Bowers, Y., Person
'B', Smaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Rittler
'E', Korn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R., and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu

FEATURES
source
1..91
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:353602"
/clone_1lb="Soares mouse embryo NDME13.5 14.5"
/issue_type="unknown"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
'GTTCACCACTGAGAGTGGAGCGCGCGAATTTTATTTTATTTTATTTT
T3'] on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2]: double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified

p773 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M. Fatima Bonaldo."

BASE COUNT 25 a 19 c 14 g 33 t
ORIGIN
Query Match 0.5%; Score 25.8; DB 9; Length 91;
Best Local Similarity 67.9%; Pred. No. 9.4e+04;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

RESULT 33
A1794139/c 100 bp mRNA linear EST 27-JUN-2002
LOCUS
DEFINITION
A1794139 XGC-neurula Silurana tropicalis cDNA clone TNeu16ml3 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
western clawed frog.
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 100)
Taylor, R., Ashurst, J.L., Cronling, M.D.R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2002
Unpublished (2001)
Contact: Taylor R
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE.ID: TNeu16ml3.plcsp6
Sequencing primer: PLCSP6
This sequence is from a Xenopus gene collection (XGC) library
constructed by Aaron M. Zorn.

FEATURES
source
1..100
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone_1lb="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."

BASE COUNT 17 a 15 c 18 g 50 t
ORIGIN
Query Match 0.5%; Score 25.8; DB 9; Length 100;
Best Local Similarity 67.9%; Pred. No. 9.7e+04;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

RESULT 34
A1142956 73 bp mRNA linear EST 25-SEP-1998
LOCUS
DEFINITION
A1142956 O11 Soares senescent fibroblasts_NBHSF Homo sapiens CDNA
clone IMAGE:1679521 3' similar to SW:SR54_HUMAN P13624 SIGNAL
RECOGNITION PARTICLE 54 KD PROTEIN ; mRNA sequence.
ACCESSION
VERSION
A1142956.1 GI:3659315

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 05:35:07 ; Search time 630 Seconds

(without alignments)
17837.257 Million cell updates/sec

Title: US-09-676-436-3

Sequence: 1 ctagaagactctccgatga.....ggtattatcttagaagctc 4990

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2389434

Minimum DB seq length: 8

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

N_Geneseq_101002: *
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT: *
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT: *
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT: *
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5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT: *
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9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT: *
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11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT: *
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21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT: *
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT: *
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: *
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	1.2	60	24	ABN55465
2	44.8	0.9	65	24	ABN55482
3	28	0.6	78	24	AAD37143
4	27.2	0.5	78	18	AAT50934
5	26.6	0.5	92	21	AA019445
6	26	0.5	26	24	AAD37145
7	26	0.5	100	16	AA066400
8	25.8	0.5	81	24	ABK53302
9	25.2	0.5	60	22	AAH48689

10	25.2	0.5	70	21	AAA71594	Human brain natrin
11	25.2	0.5	89	16	AAT22086	Human gene signatu
12	25.2	0.5	99	18	AAT92244	Mercuric ion reduc
13	25.2	0.5	20	21	AA228594	Primer 307-3395 fo
14	25	0.5	59	20	AAA73946	GFP Leu(CTG)5 forw
15	25	0.5	91	22	ABA69691	Human foetal olig
16	25	0.5	96	24	ABL58788	Synthetic GFP olig
17	24.8	0.5	77	21	AA012392	Human secreted pro
18	24.8	0.5	92	22	AA506930	Reverse PCR primer
19	24.8	0.5	94	21	AA011499	Human secreted pro
20	24.8	0.5	94	21	AA015541	Human secreted pro
21	24.8	0.5	65	24	ABN54107	Mouse spliced tran
22	24.8	0.5	71	18	AA065208	Transforming growt
23	24.8	0.5	72	21	AA52344	cDNA encoding Dros
24	24.6	0.5	72	24	ABK36568	HCY DNA encoding H
25	24.6	0.5	98	20	AA023428	Human neutrophil c
26	24.4	0.5	82	20	AA023428	80Kc Bundle peptid
27	24.4	0.5	99	22	ABK68815	Human foetal liver
28	24.4	0.5	99	22	ABK35588	Probe #14054 for g
29	24.4	0.5	100	16	AA086411	Human insulin deri
30	24.2	0.5	80	22	ABK72801	Human foetal liver
31	24.2	0.5	80	22	AAK21231	Human brain expres
32	24.2	0.5	80	22	AAK47388	Human bone marrow
33	24.2	0.5	80	22	AAK53226	Probe #21912 used
34	24.2	0.5	84	21	AAA92397	Thymosin alpha-1 n
35	24.2	0.5	90	24	ABK36388	HIV DNA encoding G
36	24.2	0.5	94	21	AAH51645	Sbgl exon sequence
37	24.2	0.5	94	21	AAH51668	Sbgl exon sequence
38	24.2	0.5	94	21	AAH51692	Sbgl exon sequence
39	24.2	0.5	95	22	ABK71915	Human foetal liver
40	24.2	0.5	95	22	AAK20302	Human brain expres
41	24.2	0.5	95	22	AAK46381	Human bone marrow
42	24.2	0.5	95	22	AA152270	Probe #20956 used
43	24.2	0.5	95	22	ABK52072	Human genome deriv
44	24.2	0.5	99	22	ABA755243	Human foetal liver
45	24.2	0.5	99	22	ABA39902	Probe #18968 for g
46	24.2	0.5	99	22	AAK39875	Human brain expres
47	24.2	0.5	99	22	AAK47987	Human bone marrow
48	24.2	0.5	99	22	AAK26980	Human bone marrow
49	24.2	0.5	99	22	AA126980	Probe #16913 for g
50	24.2	0.5	99	22	AA126980	Probe #24484 used
51	24	0.5	99	22	AA037144	Human MEK4 DNA am
52	24	0.5	99	22	ABN52352	Human spliced tran
53	24	0.5	65	24	ABN57019	Mouse spliced tran
54	24	0.5	66	22	ABN57019	Mouse spliced tran
55	24	0.5	78	24	AA037278	Synthetic transcri
56	24	0.5	97	14	AA037278	Cell death protect
57	24	0.5	97	14	AA037278	Clone 92-2 used. In
58	24	0.5	97	16	AA094997	SSP 5.11.11.5 clon
59	24	0.5	97	19	AA094997	Synthetic storage
60	24	0.5	97	20	AAV95835	Human SNP oligonuc
61	23.8	0.5	51	22	AA131772	Human SNP oligonuc
62	23.8	0.5	65	24	ABN51688	Mouse spliced tran
63	23.8	0.5	83	19	AAV31043	Expression vector
64	23.8	0.5	90	22	ABK70244	Human foetal liver
65	23.8	0.5	90	22	AAK36968	Probe #15434 for g
66	23.8	0.5	90	22	AAK18470	Human brain expres
67	23.8	0.5	90	22	AAK4379	Human bone marrow
68	23.8	0.5	90	22	AA124842	Probe #14775 for g
69	23.8	0.5	90	22	AA150375	Probe #19061 used
70	23.8	0.5	90	22	ABK58614	Human genome deriv
71	23.8	0.5	93	16	AA082238	Sequence encoding
72	23.8	0.5	93	16	AA171971	Human gene signatu
73	23.8	0.5	94	24	ABK17274	Coupled ligation a
74	23.6	0.5	94	24	ABK17311	Coupled ligation a
75	23.6	0.5	60	22	ABK48688	Human G-protein su
76	23.6	0.5	60	22	ABN42052	Human spliced tran
77	23.6	0.5	62	16	AA0720953	Human gene signatu
78	23.6	0.5	65	24	ABN53603	Mouse spliced tran
79	23.6	0.5	65	24	ABN56374	Mouse spliced tran
80	23.6	0.5	71	21	AA021184	Human secreted pro
81	23.6	0.5	82	21	AA021238	Human secreted pro
82	23.6	0.5	98	24	ABK17243	Coupled ligation a

C 229	22.2	0.4	75	22	ABAT3674	Human foetal liver	302	21.8	0.4	72	22	AA51198	Antibody variable
C 230	22.2	0.4	75	22	ABAT3898	Probe #17364 for g	C 303	21.8	0.4	77	24	ABK54849	Human colon cancer
C 231	22.2	0.4	75	22	AAK22121	Human brain expres	C 304	21.8	0.4	78	13	AA021847	PEX2A/II (Asp16->A
C 232	22.2	0.4	75	22	AAK48288	Human bone marrow	C 305	21.8	0.4	79	20	AAK86611	PCR primer Orig1084
C 233	22.2	0.4	75	22	AAI26190	Probe #16123 for g	C 306	21.8	0.4	81	19	AAV32124	HLI9, antisense ch
C 234	22.2	0.4	75	22	AAI54113	Human genome-deriv	C 307	21.8	0.4	81	19	AAV32174	HLI9, antisense ch
C 235	22.2	0.4	75	22	AB522150	DNA coding for the	C 308	21.8	0.4	82	21	AAV32174	HLI9, antisense ch
C 236	22.2	0.4	75	22	AAZ99661	Human foetal liver	C 309	21.8	0.4	82	21	AB50653	Human breast cell
C 237	22.2	0.4	83	22	ABAT70805	Probe #15750 for g	C 310	21.8	0.4	90	22	AB50653	Human breast cell
C 238	22.2	0.4	83	22	AAK19061	Human bone marrow	C 311	21.8	0.4	90	22	AB50653	Human breast cell
C 239	22.2	0.4	83	22	AAK45015	Human bone marrow	C 312	21.8	0.4	90	22	AB50653	Human breast cell
C 240	22.2	0.4	83	22	AAI25106	Probe #15039 for g	C 313	21.8	0.4	90	22	AB50653	Human breast cell
C 241	22.2	0.4	83	22	AAI25082	Probe #19668 used	C 314	21.8	0.4	90	22	AB50653	Human breast cell
C 242	22.2	0.4	83	22	AB519261	Human genome-deriv	C 315	21.8	0.4	90	22	AB50653	Human breast cell
C 243	22.2	0.4	83	22	AAI25082	Human genome-deriv	C 316	21.8	0.4	90	22	AB50653	Human breast cell
C 244	22.2	0.4	85	18	AAI25082	Human genome-deriv	C 317	21.8	0.4	90	22	AB50653	Human breast cell
C 245	22.2	0.4	87	16	AAI25082	Human genome-deriv	C 318	21.8	0.4	90	22	AB50653	Human breast cell
C 246	22.2	0.4	87	17	AAI25082	Human genome-deriv	C 319	21.8	0.4	90	22	AB50653	Human breast cell
C 247	22.2	0.4	87	17	AAI25082	Human genome-deriv	C 320	21.8	0.4	90	22	AB50653	Human breast cell
C 248	22.2	0.4	94	24	ABAT70805	Human bone marrow	C 321	21.8	0.4	90	22	AB50653	Human breast cell
C 249	22.2	0.4	94	24	ABAT70805	Human bone marrow	C 322	21.8	0.4	90	22	AB50653	Human breast cell
C 250	22.2	0.4	94	24	ABAT70805	Human bone marrow	C 323	21.8	0.4	90	22	AB50653	Human breast cell
C 251	22.2	0.4	97	21	AAI25082	Human genome-deriv	C 324	21.8	0.4	90	22	AB50653	Human breast cell
C 252	22.2	0.4	97	21	AAI25082	Human genome-deriv	C 325	21.8	0.4	90	22	AB50653	Human breast cell
C 253	22.2	0.4	99	22	AAH84217	Human secreted pro	C 326	21.8	0.4	90	22	AB50653	Human breast cell
C 254	22.2	0.4	99	22	AAH84217	Human secreted pro	C 327	21.8	0.4	90	22	AB50653	Human breast cell
C 255	22.2	0.4	99	22	AAH84217	Human secreted pro	C 328	21.8	0.4	90	22	AB50653	Human breast cell
C 256	22.2	0.4	100	14	ABAT70805	Human secreted pro	C 329	21.8	0.4	90	22	AB50653	Human breast cell
C 257	22.2	0.4	100	14	ABAT70805	Human secreted pro	C 330	21.8	0.4	90	22	AB50653	Human breast cell
C 258	22.2	0.4	51	22	AAI27973	Fuzzy C3d gene fra	C 331	21.8	0.4	90	22	AB50653	Human breast cell
C 259	22.2	0.4	53	24	ABAT70805	Human secreted pro	C 332	21.8	0.4	90	22	AB50653	Human breast cell
C 260	22.2	0.4	53	24	ABAT70805	Human secreted pro	C 333	21.8	0.4	90	22	AB50653	Human breast cell
C 261	22.2	0.4	58	16	AAI27973	Human secreted pro	C 334	21.8	0.4	90	22	AB50653	Human breast cell
C 262	22.2	0.4	64	24	AAI27973	Human secreted pro	C 335	21.8	0.4	90	22	AB50653	Human breast cell
C 263	22.2	0.4	64	24	AAI27973	Human secreted pro	C 336	21.8	0.4	90	22	AB50653	Human breast cell
C 264	22.2	0.4	65	24	AAI27973	Human secreted pro	C 337	21.8	0.4	90	22	AB50653	Human breast cell
C 265	22.2	0.4	65	24	AAI27973	Human secreted pro	C 338	21.8	0.4	90	22	AB50653	Human breast cell
C 266	22.2	0.4	65	24	AAI27973	Human secreted pro	C 339	21.8	0.4	90	22	AB50653	Human breast cell
C 267	22.2	0.4	65	24	AAI27973	Human secreted pro	C 340	21.8	0.4	90	22	AB50653	Human breast cell
C 268	22.2	0.4	65	24	AAI27973	Human secreted pro	C 341	21.8	0.4	90	22	AB50653	Human breast cell
C 269	22.2	0.4	65	24	AAI27973	Human secreted pro	C 342	21.8	0.4	90	22	AB50653	Human breast cell
C 270	22.2	0.4	65	24	AAI27973	Human secreted pro	C 343	21.8	0.4	90	22	AB50653	Human breast cell
C 271	22.2	0.4	65	24	AAI27973	Human secreted pro	C 344	21.8	0.4	90	22	AB50653	Human breast cell
C 272	22.2	0.4	65	24	AAI27973	Human secreted pro	C 345	21.8	0.4	90	22	AB50653	Human breast cell
C 273	22.2	0.4	65	24	AAI27973	Human secreted pro	C 346	21.8	0.4	90	22	AB50653	Human breast cell
C 274	22.2	0.4	65	24	AAI27973	Human secreted pro	C 347	21.8	0.4	90	22	AB50653	Human breast cell
C 275	22.2	0.4	65	24	AAI27973	Human secreted pro	C 348	21.8	0.4	90	22	AB50653	Human breast cell
C 276	22.2	0.4	65	24	AAI27973	Human secreted pro	C 349	21.8	0.4	90	22	AB50653	Human breast cell
C 277	22.2	0.4	65	24	AAI27973	Human secreted pro	C 350	21.8	0.4	90	22	AB50653	Human breast cell
C 278	22.2	0.4	65	24	AAI27973	Human secreted pro	C 351	21.8	0.4	90	22	AB50653	Human breast cell
C 279	22.2	0.4	65	24	AAI27973	Human secreted pro	C 352	21.8	0.4	90	22	AB50653	Human breast cell
C 280	22.2	0.4	65	24	AAI27973	Human secreted pro	C 353	21.8	0.4	90	22	AB50653	Human breast cell
C 281	22.2	0.4	65	24	AAI27973	Human secreted pro	C 354	21.8	0.4	90	22	AB50653	Human breast cell
C 282	22.2	0.4	65	24	AAI27973	Human secreted pro	C 355	21.8	0.4	90	22	AB50653	Human breast cell
C 283	22.2	0.4	65	24	AAI27973	Human secreted pro	C 356	21.8	0.4	90	22	AB50653	Human breast cell
C 284	22.2	0.4	65	24	AAI27973	Human secreted pro	C 357	21.8	0.4	90	22	AB50653	Human breast cell
C 285	22.2	0.4	65	24	AAI27973	Human secreted pro	C 358	21.8	0.4	90	22	AB50653	Human breast cell
C 286	22.2	0.4	65	24	AAI27973	Human secreted pro	C 359	21.8	0.4	90	22	AB50653	Human breast cell
C 287	22.2	0.4	65	24	AAI27973	Human secreted pro	C 360	21.8	0.4	90	22	AB50653	Human breast cell
C 288	22.2	0.4	65	24	AAI27973	Human secreted pro	C 361	21.8	0.4	90	22	AB50653	Human breast cell
C 289	22.2	0.4	65	24	AAI27973	Human secreted pro	C 362	21.8	0.4	90	22	AB50653	Human breast cell
C 290	22.2	0.4	65	24	AAI27973	Human secreted pro	C 363	21.8	0.4	90	22	AB50653	Human breast cell
C 291	22.2	0.4	65	24	AAI27973	Human secreted pro	C 364	21.8	0.4	90	22	AB50653	Human breast cell
C 292	22.2	0.4	65	24	AAI27973	Human secreted pro	C 365	21.8	0.4	90	22	AB50653	Human breast cell
C 293	22.2	0.4	65	24	AAI27973	Human secreted pro	C 366	21.8	0.4	90	22	AB50653	Human breast cell
C 294	22.2	0.4	65	24	AAI27973	Human secreted pro	C 367	21.8	0.4	90	22	AB50653	Human breast cell
C 295	22.2	0.4	65	24	AAI27973	Human secreted pro	C 368	21.8	0.4	90	22	AB50653	Human breast cell
C 296	22.2	0.4	65	24	AAI27973	Human secreted pro	C 369	21.8	0.4	90	22	AB50653	Human breast cell
C 297	22.2	0.4	65	24	AAI27973	Human secreted pro	C 370	21.8	0.4	90	22	AB50653	Human breast cell
C 298	22.2	0.4	65	24	AAI27973	Human secreted pro	C 371	21.8	0.4	90	22	AB50653	Human breast cell
C 299	22.2	0.4	65	24	AAI27973	Human secreted pro	C 372	21.8	0.4	90	22	AB50653	Human breast cell
C 300	22.2	0.4	65	24	AAI27973	Human secreted pro	C 373	21.8	0.4	90	22	AB50653	Human breast cell
C 301	22.2	0.4	65	24	AAI27973	Human secreted pro	C 374	21.8	0.4	90	22	AB50653	Human breast cell

C 521	21	0.4	56	16	AAT39297	Human gene signatu	C 594	21	0.4	91	22	AA154552	Probe #2328 used
C 522	21	0.4	56	17	AAT39959	Human gene signatu	C 595	21	0.4	91	22	AB522442	Human gene signatu
C 523	21	0.4	60	18	AAT96762	Human gene signatu	C 596	21	0.4	92	22	AB536575	Probe #15041 for g
C 524	21	0.4	60	18	AAT96762	Human gene signatu	C 597	21	0.4	93	22	AA110051	Probe #10042 used
C 525	21	0.4	60	21	AAZ37452	Coding sequence fo	C 598	21	0.4	93	22	ABN71460	Streptococcus poly
C 526	21	0.4	60	24	ABN36303	Human spliced tran	C 599	21	0.4	94	21	AA669951	Human ovarian carc
C 527	21	0.4	60	24	ABN41844	Human spliced tran	C 600	21	0.4	94	21	ABN72845	Ovarian carcinoma
C 528	21	0.4	60	24	ABN42991	Human spliced tran	C 601	21	0.4	96	24	ABN71374	Streptococcus poly
C 529	21	0.4	60	24	ABN45198	Human spliced tran	C 602	21	0.4	97	21	AAAC2697	Human secreted pro
C 530	21	0.4	60	24	ABN48242	Human spliced tran	C 603	21	0.4	98	20	AAO81660	bpfg binding oligo
C 531	21	0.4	60	24	ABN49150	Human spliced tran	C 604	21	0.4	98	20	AAO00174	Porcine reproduci
C 532	21	0.4	65	24	ABN29232	Rat spliced trans	C 605	21	0.4	98	22	AAAF33053	Plasmod PONY85 mt
C 533	21	0.4	65	24	ABN30612	Rat spliced trans	C 606	21	0.4	99	22	AAAC26099	Human secreted pro
C 534	21	0.4	65	24	ABN31661	Rat spliced trans	C 607	21	0.4	99	22	ABN70107	Human foetal liver
C 535	21	0.4	65	24	ABN31725	Rat spliced trans	C 608	21	0.4	99	22	ABN36893	Probe #15359 for g
C 536	21	0.4	65	24	ABN51863	Mouse spliced tran	C 609	21	0.4	99	22	AAK18322	Human brain expres
C 537	21	0.4	65	24	ABN57128	Mouse spliced tran	C 610	21	0.4	99	22	AAK44221	Human bone marrow
C 538	21	0.4	65	24	ABN57128	Mouse spliced tran	C 611	21	0.4	99	22	AA124784	Probe #14717 for g
C 539	21	0.4	66	22	AAAD14475	Anti-Her-2 Fab-2C4	C 612	21	0.4	99	22	AA150226	Human genome-deriv
C 540	21	0.4	66	22	AAAD14475	Anti-Her-2 Fab-2C4	C 613	21	0.4	99	22	AB518457	Human colon cancer
C 541	21	0.4	73	22	AAAS3697	Corneodesmosin sin	C 614	21	0.4	99	22	AB508050	Human gene signatu
C 542	21	0.4	73	22	AAAS3697	3' transmembrane r	C 615	21	0.4	100	21	AAAB0303	Sequence of cDNA c
C 543	21	0.4	74	13	AAO35851	PCR primer PCR14M	C 616	21	0.4	47	21	AAZ65527	Human map-related
C 544	21	0.4	75	21	AAO35851	Oligonucleotide SE	C 617	21	0.4	48	21	ABN75044	Human PHL3 -1 cDN
C 545	21	0.4	75	21	AAO35851	48bp i-antigen cDN	C 618	21	0.4	48	21	ABN75044	Human PHL3 -1 cDN
C 546	21	0.4	77	21	AAO35851	Human breast cell	C 619	21	0.4	49	21	ABN75044	Human PHL3 -1 cDN
C 547	21	0.4	77	21	AAO35851	Human foetal liver	C 620	21	0.4	50	21	AAH89797	Human coding sequ
C 548	21	0.4	77	21	AAO35851	Human foetal liver	C 621	21	0.4	51	21	AAH89797	Human gene signatu
C 549	21	0.4	77	21	AAO35851	Human foetal liver	C 622	21	0.4	51	21	AAH89797	Human gene signatu
C 550	21	0.4	77	21	AAO35851	Human foetal liver	C 623	21	0.4	51	21	AAH89797	Human gene signatu
C 551	21	0.4	77	21	AAO35851	Human foetal liver	C 624	21	0.4	51	21	AAH89797	Human gene signatu
C 552	21	0.4	77	21	AAO35851	Human foetal liver	C 625	21	0.4	51	21	AAH89797	Human gene signatu
C 553	21	0.4	77	21	AAO35851	Human foetal liver	C 626	21	0.4	51	21	AAH89797	Human gene signatu
C 554	21	0.4	77	21	AAO35851	Human foetal liver	C 627	21	0.4	51	21	AAH89797	Human gene signatu
C 555	21	0.4	78	22	AAH84297	Human cell death p	C 628	21	0.4	51	21	AAH89797	Human gene signatu
C 556	21	0.4	79	22	AAH84297	Human cell death p	C 629	21	0.4	51	21	AAH89797	Human gene signatu
C 557	21	0.4	79	22	AAH84297	Human cell death p	C 630	21	0.4	51	21	AAH89797	Human gene signatu
C 558	21	0.4	79	22	AAH84297	Human cell death p	C 631	21	0.4	51	21	AAH89797	Human gene signatu
C 559	21	0.4	79	22	AAH84297	Human cell death p	C 632	21	0.4	51	21	AAH89797	Human gene signatu
C 560	21	0.4	79	22	AAH84297	Human cell death p	C 633	21	0.4	51	21	AAH89797	Human gene signatu
C 561	21	0.4	79	22	AAH84297	Human cell death p	C 634	21	0.4	51	21	AAH89797	Human gene signatu
C 562	21	0.4	79	22	AAH84297	Human cell death p	C 635	21	0.4	51	21	AAH89797	Human gene signatu
C 563	21	0.4	79	22	AAH84297	Human cell death p	C 636	21	0.4	51	21	AAH89797	Human gene signatu
C 564	21	0.4	79	22	AAH84297	Human cell death p	C 637	21	0.4	51	21	AAH89797	Human gene signatu
C 565	21	0.4	79	22	AAH84297	Human cell death p	C 638	21	0.4	51	21	AAH89797	Human gene signatu
C 566	21	0.4	79	22	AAH84297	Human cell death p	C 639	21	0.4	51	21	AAH89797	Human gene signatu
C 567	21	0.4	79	22	AAH84297	Human cell death p	C 640	21	0.4	51	21	AAH89797	Human gene signatu
C 568	21	0.4	79	22	AAH84297	Human cell death p	C 641	21	0.4	51	21	AAH89797	Human gene signatu
C 569	21	0.4	79	22	AAH84297	Human cell death p	C 642	21	0.4	51	21	AAH89797	Human gene signatu
C 570	21	0.4	79	22	AAH84297	Human cell death p	C 643	21	0.4	51	21	AAH89797	Human gene signatu
C 571	21	0.4	79	22	AAH84297	Human cell death p	C 644	21	0.4	51	21	AAH89797	Human gene signatu
C 572	21	0.4	79	22	AAH84297	Human cell death p	C 645	21	0.4	51	21	AAH89797	Human gene signatu
C 573	21	0.4	79	22	AAH84297	Human cell death p	C 646	21	0.4	51	21	AAH89797	Human gene signatu
C 574	21	0.4	79	22	AAH84297	Human cell death p	C 647	21	0.4	51	21	AAH89797	Human gene signatu
C 575	21	0.4	79	22	AAH84297	Human cell death p	C 648	21	0.4	51	21	AAH89797	Human gene signatu
C 576	21	0.4	79	22	AAH84297	Human cell death p	C 649	21	0.4	51	21	AAH89797	Human gene signatu
C 577	21	0.4	79	22	AAH84297	Human cell death p	C 650	21	0.4	51	21	AAH89797	Human gene signatu
C 578	21	0.4	79	22	AAH84297	Human cell death p	C 651	21	0.4	51	21	AAH89797	Human gene signatu
C 579	21	0.4	79	22	AAH84297	Human cell death p	C 652	21	0.4	51	21	AAH89797	Human gene signatu
C 580	21	0.4	79	22	AAH84297	Human cell death p	C 653	21	0.4	51	21	AAH89797	Human gene signatu
C 581	21	0.4	79	22	AAH84297	Human cell death p	C 654	21	0.4	51	21	AAH89797	Human gene signatu
C 582	21	0.4	79	22	AAH84297	Human cell death p	C 655	21	0.4	51	21	AAH89797	Human gene signatu
C 583	21	0.4	79	22	AAH84297	Human cell death p	C 656	21	0.4	51	21	AAH89797	Human gene signatu
C 584	21	0.4	79	22	AAH84297	Human cell death p	C 657	21	0.4	51	21	AAH89797	Human gene signatu
C 585	21	0.4	79	22	AAH84297	Human cell death p	C 658	21	0.4	51	21	AAH89797	Human gene signatu
C 586	21	0.4	79	22	AAH84297	Human cell death p	C 659	21	0.4	51	21	AAH89797	Human gene signatu
C 587	21	0.4	79	22	AAH84297	Human cell death p	C 660	21	0.4	51	21	AAH89797	Human gene signatu
C 588	21	0.4	79	22	AAH84297	Human cell death p	C 661	21	0.4	51	21	AAH89797	Human gene signatu
C 589	21	0.4	79	22	AAH84297	Human cell death p	C 662	21	0.4	51	21	AAH89797	Human gene signatu
C 590	21	0.4	79	22	AAH84297	Human cell death p	C 663	21	0.4	51	21	AAH89797	Human gene signatu
C 591	21	0.4	79	22	AAH84297	Human cell death p	C 664	21	0.4	51	21	AAH89797	Human gene signatu
C 592	21	0.4	79	22	AAH84297	Human cell death p	C 665	21	0.4	51	21	AAH89797	Human gene signatu
C 593	21	0.4	79	22	AAH84297	Human cell death p	C 666	21	0.4	51	21	AAH89797	Human gene signatu

813	20.6	0.4	77	21	AA29105	Human secreted pro	C 886	20.6	0.4	100	24	AB20222	Human genome-deriv
814	20.6	0.4	77	21	AA29301	Sense primer for i	C 887	20.4	0.4	45	18	AAV03162	Biotinylated inter
815	20.6	0.4	78	19	AAV6244	Humanized antibody	C 888	20.4	0.4	45	18	ABN84053	Class II MHC I-Ag7
816	20.6	0.4	78	19	AAV32118	LH13 antisense ch	C 889	20.4	0.4	47	21	AA269017	Human map-related
817	20.6	0.4	78	19	AAV32126	LH13 antisense hu	C 890	20.4	0.4	50	22	AA300022	Human secreted pro
818	20.6	0.4	78	19	AAV32168	LH21 antisense hu	C 891	20.4	0.4	50	22	AA130441	Human SNP oligonuc
819	20.6	0.4	78	19	AAV32176	Oligonucleotide 4	C 892	20.4	0.4	51	22	ABN71624	Streptococcus agal
820	20.6	0.4	78	20	AA101175	Bacillus sp. GUS g	C 893	20.4	0.4	51	22	AA175214	Human silent SNP c
821	20.6	0.4	80	20	AA233805	Secreted microb	C 894	20.4	0.4	54	21	AA179463	Human silent SNP c
822	20.6	0.4	80	21	AA29397	HIV-1 reverse tran	C 895	20.4	0.4	54	21	AA23240	Human protective D
823	20.6	0.4	81	16	AA206222	L-selectin family	C 896	20.4	0.4	57	15	AA057878	Schistosoma manso
824	20.6	0.4	81	18	AA207930	Primer CD-3-10 use	C 897	20.4	0.4	57	15	AA057879	Schistosoma manso
825	20.6	0.4	81	21	AA237368	Cornedestoin sin	C 898	20.4	0.4	57	19	AAV20390	Primer 7 for human
826	20.6	0.4	82	22	AA243746	Probe #19197 for g	C 899	20.4	0.4	59	17	AA216654	Trichoderma reesei
827	20.6	0.4	82	22	AA240731	Human brain expres	C 900	20.4	0.4	59	21	AA234222	PAPF1-TfeAF gene
828	20.6	0.4	82	22	AA240838	Human bone marrow	C 901	20.4	0.4	60	21	AA234222	RNA clone 21.08 fo
829	20.6	0.4	82	24	AA243338	Human genome-deriv	C 902	20.4	0.4	60	21	AA234222	Human spliced tran
830	20.6	0.4	84	22	AA243338	Human breast cell	C 903	20.4	0.4	60	24	ABN33736	Human spliced tran
831	20.6	0.4	84	22	AB243144	Human foetal liver	C 904	20.4	0.4	60	24	ABN35460	Human spliced tran
832	20.6	0.4	84	22	AB243144	Human foetal liver	C 905	20.4	0.4	60	24	ABN35460	Human spliced tran
833	20.6	0.4	84	22	AB243144	Human foetal liver	C 906	20.4	0.4	60	24	ABN35460	Human spliced tran
834	20.6	0.4	84	22	AB243144	Human foetal liver	C 907	20.4	0.4	60	24	ABN35460	Human spliced tran
835	20.6	0.4	84	22	AB243144	Human foetal liver	C 908	20.4	0.4	60	24	ABN35460	Human spliced tran
836	20.6	0.4	84	22	AB243144	Human foetal liver	C 909	20.4	0.4	60	24	ABN35460	Human spliced tran
837	20.6	0.4	84	22	AB243144	Human foetal liver	C 910	20.4	0.4	60	24	ABN35460	Human spliced tran
838	20.6	0.4	84	22	AB243144	Human foetal liver	C 911	20.4	0.4	60	24	ABN35460	Human spliced tran
839	20.6	0.4	84	22	AB243144	Human foetal liver	C 912	20.4	0.4	60	24	ABN35460	Human spliced tran
840	20.6	0.4	84	22	AB243144	Human foetal liver	C 913	20.4	0.4	60	24	ABN35460	Human spliced tran
841	20.6	0.4	84	22	AB243144	Human foetal liver	C 914	20.4	0.4	60	24	ABN35460	Human spliced tran
842	20.6	0.4	84	22	AB243144	Human foetal liver	C 915	20.4	0.4	60	24	ABN35460	Human spliced tran
843	20.6	0.4	84	22	AB243144	Human foetal liver	C 916	20.4	0.4	60	24	ABN35460	Human spliced tran
844	20.6	0.4	84	22	AB243144	Human foetal liver	C 917	20.4	0.4	60	24	ABN35460	Human spliced tran
845	20.6	0.4	84	22	AB243144	Human foetal liver	C 918	20.4	0.4	60	24	ABN35460	Human spliced tran
846	20.6	0.4	84	22	AB243144	Human foetal liver	C 919	20.4	0.4	60	24	ABN35460	Human spliced tran
847	20.6	0.4	84	22	AB243144	Human foetal liver	C 920	20.4	0.4	60	24	ABN35460	Human spliced tran
848	20.6	0.4	84	22	AB243144	Human foetal liver	C 921	20.4	0.4	60	24	ABN35460	Human spliced tran
849	20.6	0.4	84	22	AB243144	Human foetal liver	C 922	20.4	0.4	60	24	ABN35460	Human spliced tran
850	20.6	0.4	84	22	AB243144	Human foetal liver	C 923	20.4	0.4	60	24	ABN35460	Human spliced tran
851	20.6	0.4	84	22	AB243144	Human foetal liver	C 924	20.4	0.4	60	24	ABN35460	Human spliced tran
852	20.6	0.4	84	22	AB243144	Human foetal liver	C 925	20.4	0.4	60	24	ABN35460	Human spliced tran
853	20.6	0.4	84	22	AB243144	Human foetal liver	C 926	20.4	0.4	60	24	ABN35460	Human spliced tran
854	20.6	0.4	84	22	AB243144	Human foetal liver	C 927	20.4	0.4	60	24	ABN35460	Human spliced tran
855	20.6	0.4	84	22	AB243144	Human foetal liver	C 928	20.4	0.4	60	24	ABN35460	Human spliced tran
856	20.6	0.4	84	22	AB243144	Human foetal liver	C 929	20.4	0.4	60	24	ABN35460	Human spliced tran
857	20.6	0.4	84	22	AB243144	Human foetal liver	C 930	20.4	0.4	60	24	ABN35460	Human spliced tran
858	20.6	0.4	84	22	AB243144	Human foetal liver	C 931	20.4	0.4	60	24	ABN35460	Human spliced tran
859	20.6	0.4	84	22	AB243144	Human foetal liver	C 932	20.4	0.4	60	24	ABN35460	Human spliced tran
860	20.6	0.4	84	22	AB243144	Human foetal liver	C 933	20.4	0.4	60	24	ABN35460	Human spliced tran
861	20.6	0.4	84	22	AB243144	Human foetal liver	C 934	20.4	0.4	60	24	ABN35460	Human spliced tran
862	20.6	0.4	84	22	AB243144	Human foetal liver	C 935	20.4	0.4	60	24	ABN35460	Human spliced tran
863	20.6	0.4	84	22	AB243144	Human foetal liver	C 936	20.4	0.4	60	24	ABN35460	Human spliced tran
864	20.6	0.4	84	22	AB243144	Human foetal liver	C 937	20.4	0.4	60	24	ABN35460	Human spliced tran
865	20.6	0.4	84	22	AB243144	Human foetal liver	C 938	20.4	0.4	60	24	ABN35460	Human spliced tran
866	20.6	0.4	84	22	AB243144	Human foetal liver	C 939	20.4	0.4	60	24	ABN35460	Human spliced tran
867	20.6	0.4	84	22	AB243144	Human foetal liver	C 940	20.4	0.4	60	24	ABN35460	Human spliced tran
868	20.6	0.4	84	22	AB243144	Human foetal liver	C 941	20.4	0.4	60	24	ABN35460	Human spliced tran
869	20.6	0.4	84	22	AB243144	Human foetal liver	C 942	20.4	0.4	60	24	ABN35460	Human spliced tran
870	20.6	0.4	84	22	AB243144	Human foetal liver	C 943	20.4	0.4	60	24	ABN35460	Human spliced tran
871	20.6	0.4	84	22	AB243144	Human foetal liver	C 944	20.4	0.4	60	24	ABN35460	Human spliced tran
872	20.6	0.4	84	22	AB243144	Human foetal liver	C 945	20.4	0.4	60	24	ABN35460	Human spliced tran
873	20.6	0.4	84	22	AB243144	Human foetal liver	C 946	20.4	0.4	60	24	ABN35460	Human spliced tran
874	20.6	0.4	84	22	AB243144	Human foetal liver	C 947	20.4	0.4	60	24	ABN35460	Human spliced tran
875	20.6	0.4	84	22	AB243144	Human foetal liver	C 948	20.4	0.4	60	24	ABN35460	Human spliced tran
876	20.6	0.4	84	22	AB243144	Human foetal liver	C 949	20.4	0.4	60	24	ABN35460	Human spliced tran
877	20.6	0.4	84	22	AB243144	Human foetal liver	C 950	20.4	0.4	60	24	ABN35460	Human spliced tran
878	20.6	0.4	84	22	AB243144	Human foetal liver	C 951	20.4	0.4	60	24	ABN35460	Human spliced tran
879	20.6	0.4	84	22	AB243144	Human foetal liver	C 952	20.4	0.4	60	24	ABN35460	Human spliced tran
880	20.6	0.4	84	22	AB243144	Human foetal liver	C 953	20.4	0.4	60	24	ABN35460	Human spliced tran
881	20.6	0.4	84	22	AB243144	Human foetal liver	C 954	20.4	0.4	60	24	ABN35460	Human spliced tran
882	20.6	0.4	84	22	AB243144	Human foetal liver	C 955	20.4	0.4	60	24	ABN35460	Human spliced tran
883	20.6	0.4	84	22	AB243144	Human foetal liver	C 956	20.4	0.4	60	24	ABN35460	Human spliced tran
884	20.6	0.4	84	22	AB243144	Human foetal liver	C 957	20.4	0.4	60	24	ABN35460	Human spliced tran
885	20.6	0.4	84	22	AB243144	Human foetal liver	C 958	20.4	0.4	60	24	ABN35460	Human spliced tran

Seq	Length	Score	ID	Source
959	20.4	0.4	92	AAA36665
960	20.4	0.4	92	AA65406
961	20.4	0.4	93	AA65406
962	20.4	0.4	93	AAV58690
963	20.4	0.4	93	AAV58690
964	20.4	0.4	93	AAV58690
965	20.4	0.4	93	AAV58690
966	20.4	0.4	93	AAV58690
967	20.4	0.4	93	AAV58690
968	20.4	0.4	93	AAV58690
969	20.4	0.4	93	AAV58690
970	20.4	0.4	93	AAV58690
971	20.4	0.4	93	AAV58690
972	20.4	0.4	93	AAV58690
973	20.4	0.4	93	AAV58690
974	20.4	0.4	93	AAV58690
975	20.4	0.4	93	AAV58690
976	20.4	0.4	93	AAV58690
977	20.4	0.4	93	AAV58690
978	20.4	0.4	93	AAV58690
979	20.4	0.4	93	AAV58690
980	20.4	0.4	93	AAV58690
981	20.4	0.4	93	AAV58690
982	20.4	0.4	93	AAV58690
983	20.4	0.4	93	AAV58690
984	20.4	0.4	93	AAV58690
985	20.4	0.4	93	AAV58690
986	20.4	0.4	93	AAV58690
987	20.4	0.4	93	AAV58690
988	20.4	0.4	93	AAV58690
989	20.4	0.4	93	AAV58690
990	20.4	0.4	93	AAV58690
991	20.4	0.4	93	AAV58690
992	20.4	0.4	93	AAV58690
993	20.4	0.4	93	AAV58690
994	20.4	0.4	93	AAV58690
995	20.4	0.4	93	AAV58690
996	20.4	0.4	93	AAV58690
997	20.4	0.4	93	AAV58690
998	20.4	0.4	93	AAV58690
999	20.4	0.4	93	AAV58690
1000	20.4	0.4	93	AAV58690

ALIGNMENTS

RESULT 1
ABN35465 standard; DNA: 60 BP.

15-JUL-2002 (first entry)

Human spliced transcript detection oligonucleotide SEQ ID NO:8213.

Human; mouse; rat; splice transcript; detection; RNA transcript;
splice variant; transcriptome; oligonucleotide library; ss.

Homo sapiens.

20-JUL-2001: 2001WO-1B01903.
28-JUL-2000: 2000US-221607P.
02-MAY-2001: 2001US-287724P.
(COMP-) COMPUGEN INC.

Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which
selectively hybridize to mRNAs transcribed from a transcription unit of
a genome, useful for detecting tissue-, pathology-, and
developmental-specific genes.

Example 1; SEQ ID 8213; 47pp; English.

The present invention describes oligonucleotide libraries for detecting
messenger RNAs that populate a (sub-)transcriptome, where the
(sub-)transcriptome comprises messenger RNAs transcribed from multiple
transcription units that populate a genome. The library comprises
several oligonucleotides, each capable of hybridizing selectively to a
set of messenger RNAs transcribed from a given transcription unit of
the genome, which encodes one or more messenger RNA splice variants.
The oligonucleotide libraries are useful for detecting mRNAs from a
biological sample. In expression profiling studies, in qualitatively or
quantitatively characterizing the corresponding transcriptome, and in
detecting RNA transcripts and splice variants of human or animal
transcriptomes. The libraries may also be used as specialized mini
libraries to detect transcripts of a sub-transcriptome under a
detection of tissue- and pathology-specific state, and so allowing the
condition: to detect developmental specific genes such as those genes
transcripts and splice variants of a transcriptome of a patient suffering
from a particular disorder. ABN27253 to ABN5589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC N.B. The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pcl_sequences.

Sequence 60 BP; 17 A; 17 C; 10 G; 16 T; 0 other;

Query Match 1.2%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4560 ATAGCCCTTTTAACTGCAAGAGCTGACAGAGTGCACAGCTCTCTCT 4619
Db 1 ATAGCCCTTTTAACTGCAAGAGCTGACAGAGTGCACAGCTCTCTCTCT 60

RESULT 2
ABN5582/c
ID ABN5582 standard; DNA: 65 BP.

15-JUL-2002 (first entry)

Mouse spliced transcript detection oligonucleotide SEQ ID NO:28330.

Human; mouse; rat; splice transcript; detection; RNA transcript;
splice variant; transcriptome; oligonucleotide library; ss.

Mus musculus.

20-JUL-2001: 2001WO-1B01903.
28-JUL-2000: 2000US-221607P.
02-MAY-2001: 2001US-287724P.
(COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of
XX a genome, useful for detecting tissue, pathology, and
XX developmental-specific genes
XX
XX Example 1; SEQ ID 28330; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under specific pathological
XX conditions; to detect developmental specific genes; and to detect RNA
XX transcripts and splice variants of a transcriptome of a patient suffering
XX from a particular disorder. ABN27253 to ABN5589 represent
XX oligonucleotide sequences from rats, humans and mice, which are used in
XX the exemplification of the present invention.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WFO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 65 BP; 17 A; 18 C; 15 G; 15 T; 0 other;
XX
XX Query Match 0.9%; Score 44.8; DB 24; Length 65;
XX Best Local Similarity 81.2%; Pred. No. 0.0066;
XX Matches 52; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX QY 1541 ATTATGTGAGTTGTCAGACACCTTCATCTGAGAGAAATGAGTGTGTCT 1600
XX DB 65 ATTATGTGAGTTGTCAGACACCTTCCTCTGAGAGAAATGAGTGTGTCT 6
XX
XX QY 1601 GGGA 1604
XX DB 5 GAGA 2
XX
XX
XX RESULT 3
XX AAD37143
XX ID AAD37143 standard; DNA; 28 BP.
XX AC AAD37143;
XX
XX 21-AUG-2002 (first entry)
XX
XX Human MEK4 DNA amplifying forward PCR primer.
XX
XX Human; MEK4 modulation; mitogen-activated protein kinase kinase 4; MKK4;
XX MAP3K4; MAP three kinase 1; MAP/ERK kinase 4; MAPKK4; cytosolic;
XX MAP3K4; MAP three kinase 1; MAP/ERK kinase 4; MAPKK4; cytosolic;
XX anti-sense; inflammatory; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX PN WO200227033-A1.
XX PD 04-APR-2002.
XX PF 28-SEP-2001; 2001WO-US30549.

XX
XX 29-SEP-2000; 2000US-0676436.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Gaarde WA, Monia BP, Wyatt JR;
XX
XX WPI; 2002-416486/44.
XX
XX New antisense compound targeted to nucleic acid encoding
XX mitogen-activated protein kinase 4, useful for treating immunologic
XX disorder, inflammatory disorder or cancer
XX
XX Example 13; page 89; 132pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of MEK4 (also referred as mitogen-
XX activated protein kinase kinase 4; MAP3K4; MAP three kinase 1; MAP/ERK
XX kinase kinase 4; MAPKK4; MKK4). The antisense oligos are useful for
XX inhibiting the expression of MEK4 in cells or tissues. They are also
XX useful for treating an animal having a disease or condition associated
XX with MEK4 such as immunological, inflammatory, hyperproliferative
XX disorder or cancer. Sequences of the invention are also useful for
XX diagnostics, therapeutics, prophylaxis and as research reagents and kits.
XX They are also useful in antisense therapy. The present sequence is a
XX PCR primer which is used for amplifying human MEK4 DNA. This sequence
XX is used in the exemplification of the invention.
XX
XX Sequence 28 BP; 9 A; 5 C; 6 G; 8 T; 0 other;
XX
XX Query Match 0.6%; Score 28; DB 24; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 3.8e+02;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 784 ACTCTGGAACAAGATGTAGTACT 811
XX DB 1 ACTCTGGAACAAGATGTAGTACT 28
XX
XX
XX RESULT 4
XX AAT50934
XX ID AAT50934 standard; cDNA; 78 BP.
XX AC AAT50934;
XX
XX 07-APR-1997 (first entry)
XX
XX Mouse p53-recognition clone 1 5' sequence.
XX
XX p53 binding protein; Mdmx; tumour suppressor; cancer; ss.
XX
XX Mus sp.
XX
XX WO9641875-A1.
XX
XX 27-DEC-1996.
XX
XX 13-JUN-1996; 96WO-NL00239.
XX
XX 13-JUN-1995; 95EP-0201565.
XX
XX (INTR-) INTRIGENE BV.
XX PA (TITLE-) RIJSDUNIV LEIDEN.
XX
XX Jochimsen A, Shvarts A, Van Der Eb AJ;
XX
XX WPI; 1997-065462/06.
XX
XX Nucleic acid encoding p53-binding protein - which has homology to
XX PT mouse Mdm2, for use in cancer research
XX
XX PS Disclosure; Fig 2a; 30pp; English.
XX

CC The sequences of the 5' region (AA150934) and 3' region (AA150935)
 CC were detd. for cDNA clone 1, isolated from a mouse 16-day embryo
 CC cDNA library using tumour suppressor p53 as probe. The 5' and 3'
 CC regions (AA150936-37) of another clone were also detd. These
 CC sequences showed no significant homology to any known sequence
 CC submitted to several databases. A third clone (see also AA150933)
 CC coded for a p53 binding protein designated Mdmx (AA10206).
 XX

SO Sequence 78 BP; 3 A; 9 C; 22 G; 10 T; 4 other;

Query Match 0.5%; Score 27.2; DB 18; Length 78;
 Best Local Similarity 58.1%; Pred. No. 1.3e+03;

Matches 43; Conservative 2; Mismatches 29; Indels 0; Gaps 0;

OY 1122 GTATGAGGGTGCATGACAGAGAGATTAAAGAGTTGGAAAGTACGATGAGAG 1181
 Db 1 GTATGAGGTGGAGAGACAGAGTGTGTCATTAAGTCATACAGAGACGATGAGCA 60
 OY 1182 TGAGAGAGAACAAA 1195
 Db 61 TGVNGHAGACAAA 74

RESULT 5
 AAC19445/c

ID AAC19445 standard; cDNA: 92 BP.

XX AAC19445;

XX 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 23520.

KW Human: 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping; ss.

XX Homo sapiens.

PN EP1033401-A2.

XX 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 99US-0122487.

PA (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

DR WPI: 2000-500381/45.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 1: SEQ ID 23520; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.

SO Sequence 92 BP; 12 A; 9 C; 15 G; 47 T; 9 other;

Query Match 0.5%; Score 26.6; DB 21; Length 92;
 Best Local Similarity 57.1%; Pred. No. 2.3e+03;

Matches 36; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

OY 143 AAAAAATGATGCACCAATACGCTCCACATTAAGACACTGGAAACAGTGGAGAAATG 202
 Db 72 AAAAAAACAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAATG 13
 OY 203 TGG 205
 Db 12 TGG 10

RESULT 6
 AAD37145

ID AAD37145 standard; DNA; 26 BP.

XX AAD37145;

XX 21-AUG-2002 (first entry)

XX Human MEKK4 DNA amplifying PCR probe.

KW Human: MEKK4 modulation; mitogen-activated protein kinase kinase 4; MTK1;
 KM MAP3K4; MAP three kinase 1; MAP/ERK kinase 4; MAPKKK4; cytosolic;
 KM propylaxis; immunological; hyperproliferative disorder; cancer; therapy;
 KM antisense; inflammatory; PCR; probe; ss.

XX Homo sapiens.

OS Key Location/Qualifiers
 FH modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "FAM labelled thymine"

FT modified_base 26
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "TAMRA labelled guanine"

XX WO200227033-A1.

XX 04-APR-2002.

PF 28-SEP-2001; 2001WO-US30549.

PR 29-SEP-2000; 2000US-0676436.

PA (ISIS) ISIS PHARM INC.

PI Ward DT, Gaarde WA, Monia BP, Wyatt JR;

DR WPI: 2002-416486/44.

PT New antisense compound targeted to nucleic acid encoding
 PT mitogen-activated protein kinase 4, useful for treating immunologic
 PT disorder, inflammatory disorder or cancer -
 XX
 PS Example 13; Page 89; 132pp; English.

XX The present invention relates to antisense compounds, compositions and
 CC methods for modulating the expression of MEKK4 (also referred as mitogen-
 CC activated protein kinase kinase 4; MAP3K4; MAP three kinase 1; MAP/ERK
 CC kinase kinase 4; MAPKKK4; MTK1). The antisense oligos are useful for
 CC inhibiting the expression of MEKK4 in cells or tissues. They are also
 CC useful for treating an animal having a disease or condition associated
 CC with MEKK4 such as immunological, inflammatory, hyperproliferative
 CC disorder or cancer. Sequences of the invention are also useful for
 CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
 CC They are also useful in antisense therapy. The present sequence is a
 CC PCR probe which is used for amplifying human MEKK4 DNA. This sequence

XX Sequence 99 BP; 29 A; 21 C; 25 G; 24 T; 0 other;

Query Match 0.5%; Score 25.2; DB 20; Length 99;
Best Local Similarity 54.3%; Pred. No. 6.2e+03;
Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

OY 3026 ATGTCTCTACTAATGTGAGAGTGTGATGAGTACAGACCCAGTGGCCACTCAAGCAT 3085
DB 2 AAGACCCAGCTATAGTGAAGCTGTACTGCTGATTTCCATGGAAGCATTTGAAGTGC 61
OY 3086 TTGATTTCTTACAGCAATTGACCTGCTTTAT 3119
DB 62 GTGAGCATATCTCAAGCAAGCAAGTCTTATAT 95

RESULT 14
AAAT73946/c
ID AAA73946 standard; DNA: 54 BP.

AC AAA73946;

DT 06-DEC-2000 (first entry)

DE GFP Leu(CTG)5 forward primer.

KM Green fluorescent protein; GFP; reporter gene; codon utilisation;
translational efficiency; protein abundance; PCR primer; ss.

OS Synthetic.

PN WO200042215-A1.

PD 20-JUL-2000.

PF 07-JAN-2000; 2000MO-AU00008.

PR 08-JAN-1999; 99AU-0008078.

PA (UYOU) UNIV QUEENSLAND.

PI (SUNX/) SUN X.

PI Zhou J, Frazer IH;

DR WPI: 2000-499118/44.

Determining translational efficiency of codons in cells, comprising
introducing synthetic constructs with reporter genes fused in frame to
tandem repeats of the codon, and measuring expression -
Example 1; Page 183; 190pp; English.

The present sequence is a primer used to generate a synthetic gfp gene by
PCR amplification of a humanised gfp gene. A single artificial start
codon followed by a stretch of five identical codons was fused in frame
immediately upstream of a gfp coding sequence to form the synthetic gene.
The amplified fragment was cloned into the mammalian expression vector
pCMNA3, which contains SV40 ori and the CMV promoter, and was used in a
method for determining the translational efficiency of a codon in a cell.
The synthetic construct was introduced into COS-1 cells and expression of
of 64 gfp reporter constructs was made in which the gfp gene is preceded
in frame by a tandem repeat of 5 identical codons. The series covers the
entire set of isoaccepting codon triplets. Codons with a higher
translational efficiency than their corresponding synonymous codons can
be identified. These codons may then be used to replace the less
preferred codons of a polynucleotide so that there is higher protein
expression within undifferentiated epithelial cells such as COS-1 cells.

Sequence 54 BP; 9 A; 14 C; 20 G; 11 T; 0 other;

Query Match 0.5%; Score 25; DB 21; Length 54;
Best Local Similarity 69.4%; Pred. No. 4.7e+03;

Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 2732 CCAGTACCCGTCATGCGCAAAAGCTTTGGCAGAGTGAGATGATGAC 2780
DB 53 CCAGTGAACAGTCTCTCGCCCTTCTCAGCAGCAGCAGCATGTGAC 5

RESULT 15
ABA69691/c
ID ABA69691 standard; DNA: 91 BP.

AC ABA69691;

DT 01-FEB-2002 (first entry)

DE Human foetal liver single exon nucleic acid probe #17996.

KM Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001MO-US00669.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0633366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI: 2001-483447/52.

Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human foetal liver -
Claim 4; SEQ ID NO 17996; 639pp + sequence listing; English.

The invention relates to a single exon nucleic acid probe for
measuring human gene expression in a sample derived from human foetal
liver. The single exon nucleic acid probes may be used for predicting,
measuring and displaying gene expression in samples derived from human
foetal liver. The present sequence is a single exon nucleic acid
probe of the invention.

Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pat_sequences.

Sequence 91 BP; 28 A; 19 C; 13 G; 31 T; 0 other;

Query Match 0.5%; Score 25; DB 22; Length 91;
Best Local Similarity 61.5%; Pred. No. 6.7e+03;
Matches 40; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 3815 ACGAATTGAATAATTCGAGGATCAACACCCCAATCTGTTGGTATTTGGTGG 3874

DB 67 AAGAAATTAATTAATGATGAAGAACTGAACACCAATATTTGCTTATTTGGAACT 8

OY 3875 AGCTC 3879

DB 7 ATCTC 3

RESULT 16
ABL58788/c

KW	human PIV1; HPIV1; HPIV4; HPIV3; RSV; pathogen; measles; PCR primer;
KV	respiratory syncytial virus; respiratory tract infection; bovine; ss
XX	
XX	Human respiratory syncytial virus.
OS	
XX	WO200142445-A2.
PN	
XX	
XX	14-JUN-2001.
PD	
XX	
PE	08-DEC-2000; 2000WO-US33293.
XX	
XX	10-DEC-1999; 99US-0170195.
PR	10-DEC-1999; 98US-0458813.
PR	10-DEC-1999; 99US-0459062.
XX	
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	

XX	Homo sapiens.
OS	
XX	EPI033401-A2.
PN	
XX	06-SEP-2000.
PD	
XX	21-FEB-2000; 2000EP-0200610.
PF	
XX	26-FEB-1999; 99US-0122487.
PR	
XX	(GEST) GENSET.
PA	
XX	Dumas Milne Edwards J, Duclet A, Giordano J;
PI	
XX	WPI; 2000-500381/45.
DR	
XX	New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures - Claim 1; SEQ ID 15574; 71pp + CD-ROM; English.
PT	
XX	
XX	
XX	

PR 05-JUN-1995; 95US-0465594.
 PR 07-JUN-1995; 95US-0479725.
 PR 07-JUN-1995; 95US-0479783.
 XX
 PA (NEXS-) NEXSTAR PHARM INC.
 XX
 PI Gold L, Janjic N, Pagratlis N, Ringquist S, Toothman PJ;
 XX WPI: 1997-034387/03.
 DR
 XX Identification of nucleic acid ligands to TGF-beta, PDGF and hKGF
 PT using SELEX, used in the diagnosis and treatment of proliferative
 XX disorders
 PS
 PS Claim 15; Page 123; 209pp; English.
 XX
 CC The present sequence, a transforming growth factor beta-1
 CC (TGF-beta-1) binding ligand, was identified by Systematic Evolution
 CC of Ligands by Exponential enrichment (SELEX). Briefly, a candidate
 CC mixture of nucleic acids was contacted with TGF-beta-1, and nucleic
 CC acids having an increased affinity to TGF-beta-1, and nucleic
 CC the remainder of the mixture. The partitioned nucleic acids were
 CC then amplified to yield a mixture of nucleic acids enriched for
 CC sequences with higher affinity and specificity for binding to
 CC TGF-beta-1. The ligand is anti-mitogenic and may be used to inhibit
 CC epithelial cell proliferation, or in the diagnosis and treatment of
 CC TGF-beta-1 mediated pathological conditions, e.g. fibrotic
 CC conditions such as fibroids of the kidney, lung and liver and more
 CC acute conditions such as dermal scarring and restenosis.
 XX
 SQ Sequence 71 BP; 15 A; 16 C; 22 G; 18 T; 0 other;
 XX
 Query Match 0.5%; Score 24.6; DB 18; Length 71;
 Best Local Similarity 65.5%; Pred. No. 7.5e+03;
 Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 XX
 QY 3958 GAACATGATGATAGCTATTCAAAGCATCACCATTGGCATCAGCTCTCC 4012
 DB 56 GAAGACGTAGTAGTAAAGTATTAAACATACCCCTGCGCATCTCTCC 2
 XX
 RESULT 23
 ID AAA52344 standard; CDNA; 72 BP.
 XX
 AC AAA52344;
 XX
 DT 18-SEP-2000 (first entry)
 XX
 DE cDNA encoding Drosophila Doubletime (DBT) ATP binding domain.
 XX
 KW ATP binding domain; Doubletime; DBT; casein kinase family protein;
 KW serine/threonine kinase; Period; PER; phosphorylation; stability;
 KW circadian rhythm; clock; sleep disorder; depression; narcolepsy;
 KW jet lag; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN US6057129-A.
 XX
 PD 02-MAY-2000.
 XX
 PF 19-JUN-1998; 98US-0100664.
 XX
 PR 19-JUN-1998; 98US-0100664.
 XX
 PA (UVRQ) UNITV ROCKEFELLER.
 XX
 PI Young MW, Blau J, Price J, Kloss B;
 XX WPI: 2000-338602/29.
 DR P-PSDB; AAB01926.
 XX

PT Novel nucleic acids encoding clock protein, doubletime which is useful
 PT for treating disorders of circadian rhythm such as jet lag and mental
 PT disorders
 XX
 XX Claim 25; Column 71-72; 61pp; English.
 XX
 PS This sequence represents cDNA encoding the ATP binding domain of the
 CC Drosophila circadian rhythm protein Doubletime (DBT). DBT (AAB01923) is
 CC a member of the casein kinase protein family and comprises an ATP
 CC binding domain (AAB01926) and a serine/threonine kinase catalytic domain
 CC (AAB01927). It plays a role in regulating the concentration of the clock
 CC protein period (PER). PER acts together with timeless (TIM) in the
 CC mediation of the circadian rhythm. The PER protein is normally unstable
 CC in the cytoplasm, but is stabilised on heterodimerisation with TIM. The
 CC PER/TIM heterodimer translocates to the nucleus where it regulates the
 CC transcription of the per and tim genes through a negative feedback loop.
 CC Because PER/TIM heterodimers are only present in large numbers when high
 CC levels of per and tim RNA have accumulated, self-sustained oscillations
 CC are produced in the negative feedback loop. DBT plays a key role in the
 CC destabilisation of cytoplasmic PER monomers. It phosphorylates PER at
 CC several sites, with a high level of PER phosphorylation correlating
 CC with increased instability and degradation. The invention also
 CC discloses two mutant DBT proteins, DBT-S and DBT-L (AAB01924 and
 CC AAB01925, respectively). The DBT-S protein is associated with a
 CC shortened (faster) circadian rhythm, while the DBT-L protein is
 CC associated with a lengthened (slower) circadian rhythm. The DBT-S mutant
 CC appears to phosphorylate PER more rapidly than the wild-type protein,
 CC resulting in the premature degradation of monomeric PER. The action
 CC of DBT-L causes hypophosphorylation and persistence of monomeric PER in
 CC the cytoplasm. DBT, DBT mutants, nucleotides encoding them, DBT agonists
 CC and antagonists may be used in the prevention and/or treatment of
 CC circadian rhythm disorders including depression, narcolepsy, jet lag, and
 CC other sleep-wake cycle mental disorders.
 XX
 SQ Sequence 72 BP; 18 A; 19 C; 23 G; 12 T; 0 other;
 XX
 Query Match 0.5%; Score 24.6; DB 21; Length 72;
 Best Local Similarity 59.2%; Pred. No. 7.5e+03;
 Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 XX
 QY 3694 ATTGAGAGAGCGCAGTATGGGAGAGGTGACCTGCATCAGCCGCGGAGCTG 3753
 DB 1 ATAGGATCGGCAWCTGTGGGACATCTACCTGGGACACGATCACTGGCGAGAG 60
 XX
 QY 3754 ATGGCCATGAA 3764
 DB 61 GTGGCCATCAA 71
 XX
 RESULT 24
 ID ABR36568 standard; DNA; 90 BP.
 XX
 AC ABR36568;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE HCV DNA encoding HepC1a segment 133.
 XX
 KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
 KW viral infection; human immunodeficiency virus; melanoma;
 KW bacterial infection; Salmonella; Legionella; parasitic infection;
 KW Trypanosoma; Toxoplasma; Giardia; ds.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200190197-A1.
 XX
 PD 29-NOV-2001.
 XX
 PF 25-MAY-2001; 2001MO-AU00622.
 XX
 PR 26-MAY-2000; 2000AD-0007761.
 XX

XX (AUSU) UNIV AUSTRALIAN NAT.
 PA Thomson SA, Ramshaw IA;
 XX
 XX WPI: 2002-147575/19.
 DR P-PSDB; AAU84730.
 XX
 XX New synthetic polypeptides having several different segments of at
 PT least one parent polypeptide linked together differently compared to
 PT the linkage in the parent polypeptide, for inducing immune response
 PT against a pathogen or cancer
 XX
 XX Example 2; Fig 26; 364pp; English.
 XX
 CC The invention relates to a new synthetic polypeptide (I) comprising
 CC several different segments of at least one parent polypeptide linked
 CC together in a different relationship relative to their linkage in the
 CC parent polypeptide to impede, abrogate or otherwise alter at least one
 CC function associated with the parent polypeptide and for inducing an
 CC immune response against a pathogen or cancer. Also included are a
 CC synthetic polynucleotide encoding and a computer system for
 CC designing the synthetic polypeptides. The synthetic polypeptides and
 CC polynucleotides are referred to as a vaccine. The synthetic polypeptide is
 CC useful for modulating immune responses preferably directed against a
 CC pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix,
 CC colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone
 CC liver, oesophagus, brain, testicle, uterus), as potentiating agents or
 CC compositions comprising the polypeptide may be used in the treatment or
 CC prophylaxis against viral (such as infections caused by HIV (human
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present
 CC sequence encodes a peptide derived from a parent protein used to
 CC construct a vaccine of the invention.
 XX
 XX Sequence 90 BP; 22 A; 23 C; 21 G; 24 T; 0 other;
 SQ
 Query Match 0.5%; Score 24.6; DB 24; Length 90;
 Best Local Similarity 59.2%; Pred. No. 8.8e+03;
 Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 OY 2274 CCGGAATACGACGAGATTTCAGCCAGTTCAGAGCCCTGATGTTCT 2333
 DB 80 CCAAGGACGTTGGGCAATCAGTTGGCTTCAGCCAGGTTTGAATCGTGAAGCATTCC 21
 OY 2334 GAAATCAAAAC 2344
 DB 20 CAAATCCAAATC 10
 RESULT 25
 AAX23469/c
 ID AAX23469 standard; DNA: 98 BP.
 AC AAX23469;
 XX
 DT 17-JUN-1999 (first entry)
 XX
 DE Human neutrophil cDNA clone 876.
 XX
 KM Neutrophil: gene expression profile; granulocyte; pathogen-exposed;
 KM sterile inflammatory disease; detection; therapeutic agent; human;
 KM expression modulator; pathogenic infection; cell activation; primer;
 KM global transcriptional response; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9910536-A1.
 XX

PD 04-MAR-1999.
 XX
 XX 21-AUG-1998; 98WO-US17284.
 XX
 XX 22-AUG-1997; 97US-0056844.
 XX
 XX (UYVA) UNIV YALE.
 PA
 XX Goguen J, Newburger P, Prashar Y, Weissman SM, Yerramilli SV;
 PT WPI: 1999-204678/17.
 DR
 XX
 XX Detection of pathogen exposure or sterile inflammatory disease in a
 PT subject - by comparing gene expression profiles from granulocytes
 PT of the patient and control granulocytes
 XX
 XX Example 3; Page 41; 84pp; English.
 XX
 CC This invention describes a method for the comparison of gene expression
 CC profiles from granulocytes from a test subject and from pathogen-exposed
 CC or sterile inflammatory disease granulocytes or quiescent granulocytes.
 CC The method is used to detect pathogen exposure or sterile inflammatory
 CC disease in a subject and to identify therapeutic agents that modulate
 CC expression of a gene in response to a pathogenic infection or to
 CC sterile inflammatory disease in a subject. The method tests for global
 CC transcriptional response of granulocytes during cell activation.
 XX
 XX Sequence 98 BP; 30 A; 16 C; 20 G; 32 T; 0 other;
 SQ
 Query Match 0.5%; Score 24.6; DB 20; Length 98;
 Best Local Similarity 59.2%; Pred. No. 9.3e+03;
 Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 OY 4911 GTTCTATTCGCAAGGCTGATTCGAAATTTAAGAAAGGTTCTTTTCATTAAT 4970
 DB 93 GTTATCATACATAGACCGCATGCTATTAACAAGGGGGGTTCTTTTTCATTAAAC 34
 OY 4971 GGTATTATTTA 4981
 DB 33 GTTACAAATTA 23
 RESULT 26
 AAX25128
 ID AAX25128 standard; DNA: 82 BP.
 AC AAX25128;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE 80% Bundle peptide-encoding oligonucleotide.
 XX
 KM Flavivirus; dengue virus; envelope protein; vaccine; infection;
 KM diagnosis; ds.
 XX
 OS Synthetic.
 XX
 FH key Location/Qualifiers
 FT misc-feature 82
 FT /tag= "a
 FT /note= "Single stranded overlap on complementary
 FT strand of sequence 5'-TCCA-3'"
 XX
 PN WO9906068-A2.
 XX
 XX 11-FEB-1999.
 PD
 XX 27-JUL-1998; 98WO-US15447.
 PF
 XX 31-JUL-1997; 97US-0904227.
 PR
 XX
 PA (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
 XX

PI Coller BG, Harada KE, Ivy JM, McDonnell M, Peters ID;
 XX WPI: 1999-153454/13.
 CC Recombinant dimeric flaviviral envelope vaccine - comprising a
 CC dimeric 80kE protein, useful for protecting against flavivirus,
 CC especially dengue virus infections
 XX
 PS Example 4; Page 30; 60pp; English.
 CC This double-stranded oligonucleotide was annealed to another
 CC double-stranded oligonucleotide (see AAX25127) to generate a DNA
 CC sequence encoding the C-terminal half of a linker and
 CC helix-turn-helix domain (see AA105526). This was utilised in the
 CC construction of an expression vector for secretion of
 CC non-covalently linked 80kE Bundle, where 80kE comprises a
 CC C-terminally truncated envelope (E) protein (see AA105522) of
 CC dengue virus serotype 2 strain PR159/SI, and Bundle is the linker
 CC and helix-turn-helix moiety that is designed to form a
 CC non-covalently associated 4-helix bundle domain that enhances the
 CC dimerisation of the 80kE molecule. A vaccine for protecting
 CC against DEN-2 infection comprises a dimeric 80kE protein that has
 CC been secreted as a recombinant protein from a eukaryotic cell.
 XX
 SQ Sequence 82 BP; 19 A; 19 C; 32 G; 12 T; 0 other;
 Query Match 0.5%; Score 24.4; DB 20; Length 82;
 Best Local Similarity 63.8%; Pred. No. 9.4e+03;
 Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
 QY 1789 CTGATGAGGAGTACTACGATTCATGTCGACAGGATTCGTGGAGACCTGGAGAACG 1846
 DB 1 CTGCTGAAGGGCCCCCGCAAGGCGAGCTGGAGAGACTGCTGAAGACCTGAAGAGAGC 58
 RESULT 27
 ABA68615/C
 ID ABA68615 standard; DNA; 99 BP.
 XX
 AC ABA68615;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human foetal liver single exon nucleic acid probe #16920.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200157277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00669.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 PS WPI: 2001-483447/52.
 XX
 DR Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human fetal liver
 XX
 PS Claim 4; SEQ ID NO 16920; 639bp + sequence listing; English.

XX
 CC The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a single exon nucleic acid
 CC probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 99 BP; 25 A; 14 C; 35 G; 25 T; 0 other;
 Query Match 0.5%; Score 24.4; DB 22; Length 99;
 Best Local Similarity 58.1%; Pred. No. 1.1e+04;
 Matches 43; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
 QY 751 AATGTAATGTCGATGAGGAGGCGATGCAAGGCGATGCTGCAACAAAGATTGATGTTAC 810
 DB 94 AATGTAATGTCGATGAGGAGGATCCCAAGCGCTGCGACGACCAATGATGATCTCTC 35
 QY 811 TCAACACATCATGA 824
 DB 34 TGACCTCATCATCA 21
 RESULT 28
 ABA35588/C
 ID ABA35588 standard; DNA; 99 BP.
 XX
 AC ABA35588;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Probe #14054 for gene expression analysis in human heart cell sample.
 XX
 KW Human; gene expression; heart; microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200157274-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00666.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 PS WPI: 2001-488899/53.
 XX
 DR Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts -
 XX
 PS Claim 4; SEQ ID NO 14054; 530pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC present sequence is one such probe. The probes may be used for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging,

ID AAK21231 standard; DNA; 80 BP.
 XX
 AC AAK21231;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human brain expressed single exon probe SEQ ID NO: 21222.
 XX
 KW Human; brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200157275-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00667.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483446/52.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT brains -
 XX
 PS Example 4; SEQ ID NO: 21222; 650pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system,
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention.
 CC
 SQ Sequence 80 BP; 18 A; 15 C; 13 G; 34 T; 0 other;
 CC
 Query Match 0.5%; Score 24.2; DB 22; Length 80;
 Best Local Similarity 62.3%; Pred. No. 1.1e+04;
 Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 OY 3462 AAGAAAGAGTGGGAACTTCGACATATCAGCCAGAGTAAGATGCTTCTAACT 3521
 DB 66 AAGAAATTATCAAGCACTGTGACATTTAAGGCCACAGAAATCATCTGTTATAATT 7
 OY 3522 A 3522
 DB 6 A 6
 XX
 RESULT 32
 ID AAK47388/C
 AC AAK47388 standard; DNA; 80 BP.
 XX
 AC AAK47388;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human bone marrow expressed single exon probe SEQ ID NO: 21945.
 XX
 KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukemia; lymphoma; myeloma; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200157276-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00668.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488900/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human bone marrow -
 XX
 PS Example 4; SEQ ID NO: 21945; 658pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukemia and myeloma. The present sequence is one of
 CC the probes of the invention.
 CC
 SQ Sequence 80 BP; 18 A; 15 C; 13 G; 34 T; 0 other;
 CC
 Query Match 0.5%; Score 24.2; DB 22; Length 80;
 Best Local Similarity 62.3%; Pred. No. 1.1e+04;
 Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 OY 3462 AAGAAAGAGTGGGAACTTCGACATATCAGCCAGAGTAAGATGCTTCTAACT 3521
 DB 66 AAGAAATTATCAAGCACTGTGACATTTAAGGCCACAGAAATCATCTGTTATAATT 7
 OY 3522 A 3522
 DB 6 A 6
 XX
 RESULT 33
 ID AAI53226/C
 AC AAI53226 standard; DNA; 80 BP.
 XX
 AC AAI53226;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Probe #21912 used to measure gene expression in human placenta sample.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00663.
 XX
 PR 04-FEB-2000; 2000US-0180312.

PS Claim 1: Page 568; 737pp; English.

XX AAH51601 represents a human genomic nucleotide sequence comprising sbg1,
 CC g34665, sbg2, g35017 and g35018 nucleic acid sequences located on the
 CC human chromosome 13q31-q33 locus. The nucleotide sequences contain
 CC AluI markers and polymorphisms. Sequences AAH51602 - AAH51626 and
 CC AAH51627 - AAH51631 represent cDNA sequences and protein
 CC products. AAH51632 - AAH51633 and AAH51634 represent g35018
 CC cDNA sequences and protein products. Primers AAH51632 - AAH51633 are used
 CC to isolate sbg1 cDNAs, while sbg1 exons from different primates are
 CC represented by sequences AAH51634 - AAH51639. Nucleotide sequences of
 CC amplicons which comprise AluI markers located on the chromosome
 CC 13q31-q33 locus are represented in AAH51700 - AAH51817. Biallelic markers
 CC are represented in the sequences by degenerate/undefined base codes. PCR
 CC primers AAH51818 and AAH51819 are used in the isolation of sequences of
 CC the invention. The identity of the nucleotide at a biallelic marker in
 CC a sample DNA sequence is determined by the identity of a nucleotide at a Region
 CC D-related biallelic marker in a biological sample from single or multiple
 CC subjects. By determining the frequency of a biallelic marker in a
 CC population an association between a genotype and a trait, a haplotype and
 CC a trait can be detected. The sequences can be used to determine a predisposition to or early onset of schizophrenia or
 CC bipolar disorder or a beneficial response to or side effects related to
 CC treatment against schizophrenia or bipolar disorder.

XX Sequence 94 BP; 29 A; 15 C; 20 G; 30 T; 0 other;

SO Query Match 0.5%; Score 24.2; DB 21; Length 94;
 Best Local Similarity 78.4%; Pred. No. 1.2e+04;
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1048 AAGAAATTTCTCAGATATTTGCTGGCAGCTTATGCAA 1084
 DB 46 AAGAAATTTCTCAGATATTTGCTGGCAGCTTATGCAA 82

RESULT 38
 AAH51692 standard; DNA; 94 BP.

XX AAH51692:
 AC 29-AUG-2001 (first entry)
 XX sbg1 exon sequence SEQ ID 104.
 DE sbg1; g34665; sbg2; g35017; g35018; chromosome 13q31-q33; haplotype;
 XX biallelic marker; polymorphism; schizophrenia; bipolar disorder; ds.
 KW Macaca mulatta.
 OS WO200058510-A2.
 XX 05-OCT-2000.
 PD 30-MAR-2000; 2000MO-IB00435.
 PF 30-MAR-1999; 99US-0126903.
 XX 30-APR-1999; 99US-0131971.
 PR 30-APR-1999; 99US-0132065.
 XX 1-JUL-1999; 99US-0143928.
 PR 1-JUL-1999; 99US-0145915.
 XX 2-JUL-1999; 99US-0146452.
 PR 2-JUL-1999; 99US-0146453.
 XX 28-OCT-1999; 99US-0162288.
 PR (GSEST) GENSET.
 XX Cohen D, Blumenfeld M, Chumakov I, Bougueteloret L, Bihain B;
 XX Eslioux L;

DR WPI; 2000-619082/59.

XX Polynucleotides comprising sequences from sbg1 and g35018 biallelic
 PT markers are used for genotyping and detecting schizophrenia or bipolar
 CC disorder and predisposition to these disorders.

PS Claim 1: Page 573; 737pp; English.

XX AAH51601 represents a human genomic nucleotide sequence comprising sbg1,
 CC g34665, sbg2, g35017 and g35018 nucleic acid sequences located on the
 CC human chromosome 13q31-q33 locus. The nucleotide sequences contain
 CC AluI markers and polymorphisms. Sequences AAH51602 - AAH51626 and
 CC AAH51627 - AAH51631 represent cDNA sequences and protein
 CC products. AAH51632 - AAH51633 and AAH51634 represent g35018
 CC cDNA sequences and protein products. Primers AAH51632 - AAH51633 are used
 CC to isolate sbg1 cDNAs, while sbg1 exons from different primates are
 CC represented by sequences AAH51634 - AAH51639. Nucleotide sequences of
 CC amplicons which comprise AluI markers located on the chromosome
 CC 13q31-q33 locus are represented in AAH51700 - AAH51817. Biallelic markers
 CC are represented in the sequences by degenerate/undefined base codes. PCR
 CC primers AAH51818 and AAH51819 are used in the isolation of sequences of
 CC the invention. The identity of the nucleotide at a biallelic marker in
 CC a sample DNA sequence is determined by the identity of a nucleotide at a Region
 CC D-related biallelic marker in a biological sample from single or multiple
 CC subjects. By determining the frequency of a biallelic marker in a
 CC population an association between a genotype and a trait, a haplotype and
 CC a trait can be detected. The sequences can be used to determine a predisposition to or early onset of schizophrenia or
 CC bipolar disorder or a beneficial response to or side effects related to
 CC treatment against schizophrenia or bipolar disorder.

XX Sequence 94 BP; 28 A; 16 C; 20 G; 30 T; 0 other;

SO Query Match 0.5%; Score 24.2; DB 21; Length 94;
 Best Local Similarity 78.4%; Pred. No. 1.2e+04;
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1048 AAGAAATTTCTCAGATATTTGCTGGCAGCTTATGCAA 1084
 DB 46 AAGAAATTTCTCAGATATTTGCTGGCAGCTTATGCAA 82

RESULT 39
 ABA71915/C
 ID ABA71915 standard; DNA; 95 BP.

XX ABA71915:
 AC 01-FEB-2002 (first entry)
 XX Human foetal liver single exon nucleic acid probe #20220.
 DE Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 KW Homo sapiens.
 OS WO200157277-A2.
 XX 09-AUG-2001.
 PD 30-JAN-2001; 2001WO-US00669.
 PF 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0609386.
 XX 03-AUG-2000; 2000US-0637487.
 PR 21-SEP-2000; 2000US-0236356.
 XX 27-SEP-2000; 2000US-0236356.
 PR 04-OCT-2000; 2000US-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.

